

Port, Toby

From: Swope, Sheridan
Sent: Monday, July 18, 2005 11:49 AM
To: Port, Toby
Subject: FW: 10/674,636

I do not have the results from this search request.
Was it completed?
Would you send me the results?

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Monday, July 18, 2005 11:39 AM
To: Swope, Sheridan
Subject: RE: 10/674,636

Call 22523 Toby Port.

-----Original Message-----

From: Swope, Sheridan
Sent: Monday, July 18, 2005 11:23 AM
To: STIC-Biotech/ChemLib
Subject: FW: 10/674,636

Who has this search request?

-----Original Message-----

From: Swope, Sheridan
Sent: Wednesday, June 15, 2005 3:59 PM
To: STIC-Biotech/ChemLib
Subject: 10/674,636

For 10/674,636, pls search and interference search:

SID 2 regular full-length against the AA databases

SID 2 oligo search (≥ 50 AAs) against the AA databases

THANKS!!

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E02C70 Remsen Bld (Mailbox)

T. Port

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2005, 20:19:15 ; Search time 167 Seconds
(without alignments)
1345.556 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 3079
Sequence: 1 MPQGLTSSASQWCFFLLIQP.....PLSSLTFLSLLPFFFCAP 581

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_1dDec04:*

1: geneeqp1980s:*\n2: geneeqp1990s:*\n3: geneeqp2000s:*\n4: geneeqp2001s:*\n5: geneeqp2002s:*\n6: geneeqp2003as:*\n7: geneeqp2003bs:*\n8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
1	3079	100.0	581	5	ABb79537 Human car
2	3079	100.0	581	8	ADb89094 Human uro
3	2915	94.7	575	5	ABp61004 Novel hum
4	2800	94.2	642	5	AAe25025 Human dtu
5	2900	94.2	642	8	ABM84114 Human dia
6	2607.5	84.7	581	5	ABp61005 Novel hum
7	2606	84.6	525	6	ADA54807 Human pro
8	2597.5	84.4	581	6	ABUS4639 Human NOV
9	2588.5	84.1	618	5	ADr19663 Human dtu
10	2454	79.7	469	7	ADb64065 Human pro
11	1985	64.5	542	8	ADr50145 Cat cauxi
12	1985	64.5	542	8	ADr50147 Cat cauxi
13	1780	57.8	356	5	ABp61006 Novel hum
14	1262.5	41.0	561	3	AAe20911 Rat carbo
15	1230	39.9	549	3	AAE58981 Breast an
16	1230	39.9	550	8	ADG98219 Human int
17	1230	39.9	559	4	AAE31700 Protein e
18	1230	39.9	559	4	ABUS3223 Human met
19	1230	39.9	559	6	ABE82851 CES2 rela
20	1230	39.9	559	6	AAE33960 Human pro
21	1230	39.9	559	7	ADD46521 Human car
22	1231	39.7	306	5	AAE20909 Human car
23	1213.5	39.4	561	7	ADD46519 Rat Prote
24	1191	38.7	607	4	ABUS3222 Human met
25	1186.5	38.5	554	8	ADr79890 Mouse 11v

26	1181	38.4	583	4	ABG10273	ABg10273 Novel hum
27	1179.5	38.3	571	3	AAV71107	AAV71107 Human Hyd
28	1179.5	38.3	571	4	AAU12442	AAU12442 Human PRO
29	1179.5	38.3	571	4	AAE04101	AAE04101 Human gen
30	1179.5	38.3	571	5	AAU83696	AAU83696 Human PRO
31	1179.5	38.3	571	5	ABE84949	ABE84949 Human PRO
32	1179.5	38.3	571	5	ABE64341	ABg64341 Human alb
33	1179.5	38.3	571	6	ABO17886	ABO17886 Novel hum
34	1179.5	38.3	571	6	ABU69108	ABU69108 Human PRO
35	1179.5	38.3	571	6	ABU80843	ABU80843 Human PRO
36	1179.5	38.3	571	6	ABO33809	ABO33809 Novel hum
37	1179.5	38.3	571	6	ABU81140	ABU81140 Human PRO
38	1179.5	38.3	571	6	ABO19424	ABO19424 Human sec
39	1179.5	38.3	571	6	ABU66840	ABU66840 Human PRO
40	1179.5	38.3	571	6	ABU59921	ABU59921 Novel sec
41	1179.5	38.3	571	6	ABU69085	ABU69085 Human PRO
42	1179.5	38.3	571	6	ABO25111	ABO25111 Human sec
43	1179.5	38.3	571	6	ABU82152	ABU82152 Novel hum
44	1179.5	38.3	571	6	ABU67116	ABU67116 Human sec
45	1179.5	38.3	571	6	ABU81549	ABU81549 Human sec

ALIGNMENTS

RESULT 1	ABb79537	
ID	ABb79537 standard; protein; 581 AA.	
XX		
AC	ABb79537;	
DT	23-SEP-2002 (first entry)	
XX		
DE	Human carboxylesterase family member 53010.	
XX		
KM	Carboxylesterase; enzyme; human; analgesic; nootropic; antiinflammatory;	
KW	diagnosis; therapy.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	Peptide	1..26
FT	Protein	/label= Signal_peptide
FT	Domain	27..581
FT	Region	/label= Mature_protein
FT	Active-site	44..545
FT		/note= "carboxylesterase domain"
FT		125..135
FT		/note= "predicted carboxylesterase type-B signature"
FT		219..234
FT		/note= "predicted carboxylesterase type-B serine active site"
XX		
PD	27-JUN-2002.	
XX		
PF	18-DEC-2001; 2001WO-US049075.	
XX		
PR	18-DEC-2000; 2000US-0256369P.	
XX		
PR	28-MAR-2001; 2001US-0279508P.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
XX		
PI	Curtis RAJ, Silos-Santiago I;	
XX		
DR	WPI; 2002-547936/58.	
XX		
DR	N-PSDB; AAN84302.	
XX		
PT	53010 nucleic acids, useful for diagnosing and treating e.g. vascular	
PT	diseases, autoimmune diseases, or neurodegenerative diseases, as	
XX	surrogate markers, in tissue typing and chromosome mapping.	


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Db      121 FGVEDCLYLNIYAPAHADTGSKL PVLVWFGGAFKTSASIFDGSALAAVEDLVVVVV 180
Oy      181 YRLGIFGFTTWDQHPAGNMAFKQOVAALSWQKNIIEFFGDPSSVTITFGSAGASIVSS 240
Db      181 YRLGIFGFTTWDQHPAGNMAFKQOVAALSWQKNIIEFFGDPSSVTITFGSAGASIVSS 240
Oy      241 LIISPMAGLPHKAIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDEBALICRT 300
Db      241 LIISPMAGLPHKAIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDEBALICRT 300
Oy      301 KPSKELLTSGKTSFPYVVDGAFPPNEDLLSOKAKAIPSIIGVNNHCGFLPMKE 360
Db      301 KPSKELLTSGKTSFPYVVDGAFPPNEDLLSOKAKAIPSIIGVNNHCGFLPMKE 360
Oy      361 APELISGNSKSLAHLIONIHIIPQYHLVANEYFHDKSLTEIRSDLLDLGVFFV 420
Db      361 APELISGNSKSLAHLIONIHIIPQYHLVANEYFHDKSLTEIRSDLLDLGVFFV 420
Oy      421 PALITARYHARDAGAVPYEFERHRRPQCFEDTKPAFVKADHDEVFVGAFKGDIVMF 480
Db      421 PALITARYHARDAGAVPYEFERHRRPQCFEDTKPAFVKADHDEVFVGAFKGDIVMF 480
Oy      481 EGATEEBEKLIRKMKKATPARGTGNPNGNDSLMPAVNLTEQYQLDNLMSLGRLKEP 540
Db      481 EGATEEBEKLIRKMKKATPARGTGNPNGNDSLMPAVNLTEQYQLDNLMSLGRLKEP 540
Oy      541 RVDFWTSITPILASDMHSPLSLTPSLLOPPFFCAP 581
Db      541 RVDFWTSITPILASDMHSPLSLTPSLLOPPFFCAP 581

```

RESULT 3

ABP61004 standard; protein; 575 AA.

ABP61004;

10-SEP-2002 (first entry)

Novel human protein. SEQ ID 91.

Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian; noctropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antilucer; virucide; antichyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection; wound healing disorders; atherosclerosis; Parkinson's disease; Alzheimer's disease; autoimmune disorder; haematopoietic disorder; inflammation; neoplastic disease; nervous system disorder; cardiovascular disorder; pancreatitis; respiratory disorder; hyperproliferation; systemic autoimmune disease; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy; haematological disease; metabolic disease; sperm dysfunction; thyroid disorder; hypothyroidism; brain damage; colitis; cone photo-transduction deficiency; neurological disease; stroke; angiodenesis; ovulation disorder; spinal cord; thyroid gland; heart; trachea; thymus; lymph node; muscular system; obesity; anorexia; growth abnormality; precocious puberty.

Homo sapiens.

MO200250105-A1.

27-JUN-2002.

17-DEC-2001; 2001WO-US049232.

19-DEC-2000; 2000US-0256710P.

20-DEC-2000; 2000US-0257048P.

09-JAN-2001; 2001US-0260483P.

30-JAN-2001; 2001US-0264922P.

06-FEB-2001; 2001US-0266797P.

19-MAR-2001; 2001US-0276988P.

```

PR      08-MAY-2001; 2001US-0289622P.
XX      (SMIK ) SMITHKLINE BEECHAM CORP.
PA      (SMIK ) SMITHKLINE BEECHAM PLC.
PA      (GLAX ) GLAXO GROUP LTD.
XX      Agnew P, Birkeland M, Cogswell JP, Kadnick KF, Lai Y;
PI      Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;
XX      WPI; 2002-508784/54.
DR      N-PSDB; ABQ86169.
XX
PT      Secreted proteins and polynucleotides useful as vaccines for preventing
PT      or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT      Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
XX
PS      Claim 1(a); Page 312-313; 335pp; English.
XX
CC      The invention relates to an isolated polypeptide with signal sequences
CC      which allow it to be secreted extracellularly or membrane associated. The
CC      activity of polypeptides of the invention may be described as,
CC      cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, noctropic,
CC      neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
CC      cardiant, antilucer, virucide, antichyroid, cerebroprotective, anorectic,
CC      and metabolic. Polypeptides and polynucleotides of the invention are
CC      useful in the treatment, or as a vaccine in the prevention of, cancer,
CC      wound healing disorder, infection, atherosclerosis, Parkinson's disease
CC      and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
CC      inflammation, neoplastic diseases, nervous system related disorders and
CC      cardiovascular disorders, pancreatitis, respiratory disorder,
CC      hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC      developmental abnormality, gastrointestinal ulceration, neuropathy,
CC      haematological diseases, metabolic diseases, sperm dysfunction, thyroid
CC      disorders e.g. hypothyroidism, brain damage, colitis, cone photo-
CC      transduction deficiency, neurological diseases, stroke, angiodenesis,
CC      ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC      trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC      growth abnormalities, and alleviation of precocious puberty. The
CC      sequences given in records ABP60965-ABP61019 represent novel human
CC      proteins of the invention
XX
SQ      Sequence 575 AA;
XX
Query Match          94.7%; Score 2915; DB 5; Length 575;
Best Local Similarity 97.0%; Pred. No. 2.3e-263;
Matches 553; Conservative 3; Mismatches 6; Indels 8; Gaps 1;
XX
Oy      12 WCPFLIQPLIGHROWGKTGSAGGPOGNTRLGNIQKQVTVLGSPPVNVNPLGVFPAP 71
Db      14 WAIWTLAP-----TKGPSAGGPQNRTRLGNIQKQVTVLGSPPVNVNPLGVFPAP 65
Oy      72 PLGSLRFPNPPASPMNLRATSYPNLCLONSMWLLDDQMLVHYHPKPVSEDCLYLN 131
Db      66 PLGSLRFPNPPASPMNLRATSYPNLCLONSMWLLDDQMLVHYHPKPVSEDCLYLN 125
Oy      132 IYAPAHADTGSKL PVLVWFGGAFKTSASIFDGSALAAVEDLVVVVYVRLGIFGFTT 191
Db      126 IYAPAHADTGSKL PVLVWFGGAFKTSASIFDGSALAAVEDLVVVVYVRLGIFGFTT 185
Oy      192 WDOHAPGNMAFKQOVAALSWQKNIIEFFGDPSSVTITFGSAGASIVSSLLSPMAKLF 251
Db      186 WDOHAPGNMAFKQOVAALSWQKNIIEFFGDPSSVTITFGSAGASIVSSLLSPMAKLF 245
Oy      252 HKATMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDEBALICRTKSKELLTSSQ 311
Db      246 HKATMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDEBALICRTKSKELLTSSQ 305
Oy      312 KTKSFTRVVDGAFPPNEDLLSOKAKAIPSIIGVNNHCGFLPMKEAPEILSGSNKS 371
Db      306 KTKSFTRVVDGAFPPNEDLLSOKAKAIPSIIGVNNHCGFLPMKEAPEILSGSNKS 365
Oy      372 LALHLIONIHIIPQYHLVANEYFHDKSLTEIRSDLLDLGVFFVVPALITARYHARD 431

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Db 366 LALHLIIONIIHIPQYILVLANEYFHDKSLTEIRDSLLDLGDFVFPVPLITARYRD 425
Qy 432 AGAPVTFYFEPHRRPOCFEDTKPAFVAKADHAEVRPFGGAFKGDIVWFEGATEBEKLLS 491
Db 426 AGAPVTFYFEPHRRPOCFEDTKPAFVAKADHAEVRPFGGAFKGDIVWFEGATEBEKLLS 485
Qy 492 RKMKWYATFARTGNGNDLSLMPAYNLTEQYLOLDINMSLGQRLKEPRVDFTSTIPL 551
Db 486 RKMKWYATFARTGNGNDLSLMPAYNLTEQYLOLDINMSLGQRLKEPRVDFTSTIPL 545
Qy 552 IISASDMLHSPSLTFLSLQPPFFFCAP 581
Db 546 IISASDMLHSPSLTFLSLQPPFFFCAP 575

RESULT 4
AAE25025
ID AAE25025 standard; protein; 642 AA.

AC AAE25025;

DT 30-OCT-2002 (first entry)

DE Human drug metabolizing enzyme (DME-10).

Human; drug metabolizing enzyme; autoimmune; inflammatory disorder;
acquired immunodeficiency syndrome; AIDS; atherosclerosis; psoriasis;
proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer;
dementia; Parkinson's disease; Huntington's disease;
drug screening; endocrine disorder; developmental disorder; anaemia; adenoma;
renal tubular acidosis; eye disorder; epilepsy; thrombosis; cataract;
anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder;
gout; gastrointestinal disorder; gene therapy; virocid; anticoagulant;
anticonvulsant; nootropic; enzyme; DME-10.

OS Homo sapiens.

Key Location/Qualifiers

Peptide 1..50

Domain /label=Signal_peptide

Protein /note="Transmembrane domain"

Domain /note="Mature human DME-10"

Domain /note="113..135

Domain /note="204..220

Domain /note="234..250

Domain /note="287..314

Domain /note="463..491

Domain /note="Transmembrane domain"

Domain /note="Transmembrane domain"

Domain /note="Transmembrane domain"

Domain /note="Transmembrane domain"

Domain /note="Transmembrane domain"

Domain /note="Transmembrane domain"

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Domain /note="Transmembrane domain"

Domain /note="Transmembrane domain"

Domain /note="Transmembrane domain"

Domain /note="Transmembrane domain"

Domain /note="Transmembrane domain"

Domain /note="Transmembrane domain"

PI Ison CH;
XX MPI: 2002-519668/55.
DR N-PSDB: AAD40574.
XX
PT Novel human drug metabolizing polypeptide, useful in diagnosis,
PT prevention or treatment of autoimmune/inflammatory, cell proliferative,
PT neurological, developmental, endocrine, metabolic and gastrointestinal
disorders.
XX
PS Claim 65; Page 155-156; 16pp; English.

CC The invention relates to an isolated human drug metabolizing enzyme (DME)
CC and its nucleotide. DME is useful for diagnosing, treating or preventing
CC disorders associated with aberrant expression of DME, where the disorders
CC are selected from autoimmune/inflammatory disorder such as acquired
CC immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis,
CC uveitis; a cell proliferative disorder such as arteriosclerosis,
CC cirrhosis, hepatitis, and cancer; a neurological disorder such as
CC Alzheimer's disease, Huntington's disease, dementia, Parkinson's disease;
CC a developmental disorder such as renal tubular acidosis, epilepsy,
CC anaemia; an endocrine disorder such as adenoma, thrombosis and infections
CC ; an eye disorder such as conjunctivitis, diabetes and liver disorders. DME is
CC useful in a number of drug screening techniques and to analyze the
CC proteome of a tissue or cell type. The invention is useful for creating
CC knock-in humanised animals or transgenic animals to model human diseases,
CC in somatic or germ-line gene therapy, to generate a transcript image of a
CC tissue or cell type, for detecting differences in the chromosomal
CC location due to translocation, inversion, etc. among normal, carrier or
CC affected individuals, and as hybridisation probes for mapping naturally
CC occurring genomic sequences. The present sequence is human DME-10

Sequence 642 AA:

Query Match 94.2%; Score 2900; DB 5; Length 642;
Best Local Similarity 99.5%; Pred. No. 7e-262;
Matches 548; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 31 GPSAEGPQRTLRIGWIGQVTVLGSVPVNVFLGVPAAPPLGLRFTNPQPSPMNTL 90
Db 92 GPSAEGPQRTLRIGWIGQVTVLGSVPVNVFLGVPAAPPLGLRFTNPQPSPMNTL 151
Qy 91 REATSYPNLCLQNSEMLLDDQMLKHYPKRGVSDCLYLYTPAHDGSKLPVLVWF 150
Db 152 REATSYPNLCLQNSEMLLDDQMLKHYPKRGVSDCLYLYTPAHDGSKLPVLVWF 211
Qy 151 PGGAFTGASIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQAHAGNNAFDOYVALS 210
Db 212 PGGAFTGASIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQAHAGNNAFDOYVALS 271
Qy 211 WQKNIIEFGGDPSSVTIFGESAGAISSSLILSPMAKGLFHAIWESGVAIIPYLEAHD 270
Db 272 WQKNIIEFGGDPSSVTIFGESAGAISSSLILSPMAKGLFHAIWESGVAIIPYLEAHD 331
Qy 271 YEKSEDLQVNAHFGGNNAOSEBALRLCLRTKPSKELLTJSQKTSFTRVVDGAFPNBETL 330
Db 332 YEKSEDLQVNAHFGGNNAOSEBALRLCLRTKPSKELLTJSQKTSFTRVVDGAFPNBETL 391
Qy 331 DLSQKAFKALPSIIGVNNHECGFLPMKEAPEVILSGSKSLALHLIIONIIHIPQYILH 390
Db 392 DLSQKAFKALPSIIGVNNHECGFLPMKEAPEVILSGSKSLALHLIIONIIHIPQYILH 451
Qy 391 VANEFHDKSLTEIRDSLLDLGDFVFPVPLITARYYRDGAPVYFEPHRRPOCFED 450
Db 452 VANEFHDKSLTEIRDSLLDLGDFVFPVPLITARYYRDGAPVYFEPHRRPOCFED 511
Qy 451 TKPAFVAKADHAEVRPFGGAFKGDIVWFEGATEBEKLLSRKMKWYATFARTGNGN 510
Db 512 TKPAFVAKADHAEVRPFGGAFKGDIVWFEGATEBEKLLSRKMKWYATFARTGNGN 571
Qy 511 DLSLMPAYNLTEQYLOLDINMSLGQRLKEPRVDFTSTIPLIISASDMLHSPSLTFLS 570

DB 572 DLFLMPAYNLTQYLQDLNMSLQRLKEPRVFWTSTIPILISASDMLSPSLTFLS 631
 QY 571 LLOPFFFCAP 581
 DB 632 LLOPFFFCAP 642

RESULT 5
 ABM64114
 ID ABM64114 standard; protein: 642 AA.

AC ABM64114;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4363.

XX gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

XX Homo sapiens.

XX WO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

XX Hartsbome TA, Suchorolski MT, Altus CM, Pille SJ, Elder LV;

XX Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;

XX Stevens KM, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstl EH;

XX Peralta CH, Anderson SB, Ricou P, Shen EJ, Wu MC, Stuve LL;

XX Lagace RE, Spito PA, Stewart EA, Wingrove J, Vilt UA, Kirtson ES;

XX Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX Patry S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

XX N-PSDB; ACN42766.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful

XX in diagnosing a condition, disease or disorder associated with human

XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

XX in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides

XX selected from one of the 2722 sequences defined in the specification. A

XX polynucleotide of the invention may have a use in gene therapy. The human

XX diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be

XX used to diagnose a particular condition, disease or disorder associated

XX with human molecules, e.g. cell proliferative disorders, endocrine

XX autoimmune/inflammatory disorder, developmental disorder, or

XX infections caused by virus, bacteria, fungi or parasite. The dthp

XX molecules may also be used in genetic mapping, in identifying individuals

XX from minute biological samples, in detecting single nucleotide

XX polymorphisms, as molecular weight markers, and for somatic or germline

XX gene therapy. The present sequence represents a dthp protein of the

XX invention. Note: The sequence data for this patent is not represented in

XX the printed specification, but was obtained in electronic format directly

XX from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 642 AA;

XX Query Match 94.2%; Score 2900; DB 8; Length 642;

XX Best Local Similarity 99.6%; Pred. No. 7e-262;

Matches 549; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 31 GPSAEGPQNTRLGIGKQVTVLGSVPVNVFLGVFAAPPLGSLFTNPQSPMDNL 90

DB 92 GPSAEGPQNTRLGIGKQVTVLGSVPVNVFLGVFAAPPLGSLFTNPQSPMDNL 151

QY 91 REATSYNCLQNSEWILLDQHKVHYPKYGVSEDCLYNTYPAADGSKLPVYVWF 150

DB 152 REATSYNCLQNSEWILLDQHKVHYPKYGVSEDCLYNTYPAADGSKLPVYVWF 211

QY 151 PGAFKTSASIFPGSALAAVEDLVVVOYRGIFGFTTMDQAHGNAFKDQVAALS 210

DB 212 PGAFKTSASIFPGSALAAVEDLVVVOYRGIFGFTTMDQAHGNAFKDQVAALS 271

QY 211 WVGKNIIEFPGDPSVTIIPESAGALSVSSILSPMAKGFHKAIMSGVAIIPYLEAD 270

DB 272 WVGKNIIEFPGDPSVTIIPESAGALSVSSILSPMAKGFHKAIMSGVAIIPYLEAD 331

QY 271 YEKSEDIQVVAHFCGNASDSEALLRCLRTKPSKELLTSQKTSFTRVVDGAFPPNEPL 330

DB 332 YEKSEDIQVVAHFCGNASDSEALLRCLRTKPSKELLTSQKTSFTRVVDGAFPPNEPL 391

QY 331 DLISOKAFKALPSITIGVNNHCGFLPMKEAPEILSGSNKSLAHLIONTLHIPROYLHL 390

DB 392 DLISOKAFKALPSITIGVNNHCGFLPMKEAPEILSGSNKSLAHLIONTLHIPROYLHL 451

QY 391 VANEYFHDKSLTEIRDSLLDLGDVFFVVPALITARYHDAGAPVYFEYERHRRPOCED 450

DB 452 VANEYFHDKSLTEIRDSLLDLGDVFFVVPALITARYHDAGAPVYFEYERHRRPOCED 511

QY 451 TKPAFVADNADEVRFVFGAFPLKGDIVMEGATEEKKLSRKMKTWATFARTGNNGN 510

DB 512 TKPAFVADNADEVRFVFGAFPLKGDIVMEGATEEKKLSRKMKTWATFARTGNNGN 571

QY 511 DLSTMPAYNLTQYLQDLNMSLQRLKEPRVFWTSTIPILISASDMLSPSLTFLS 570

DB 572 DLSTMPAYNLTQYLQDLNMSLQRLKEPRVFWTSTIPILISASDMLSPSLTFLS 631

QY 571 LLOPFFFCAP 581

DB 632 LLOPFFFCAP 642

RESULT 6

ABP61005

ID ABP61005 standard; protein: 581 AA.

XX ABP61005;

XX 10-SEP-2002 (first entry)

XX Novel human protein. SEQ ID 92.

XX Human; cytostatic; vulnary; antiarteriosclerotic; antiparkinsonian;

XX nootropic; neuroprotective; immunosuppressive; haemostatic;

XX antiinflammatory; cardiac; antilicer; vincide; antithyroid;

XX cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;

XX wound healing disorders; atherosclerosis; Parkinson's disease;

XX Alzheimer's disease; autoimmune disorder; hematopoietic disorder;

XX inflammation; neoplastic disease; nervous system disorder;

XX cardiovascular disorders; pancreatitis; respiratory disorder;

XX hyperproliferation; systemic autoimmune disease; hyper-immunity;

XX developmental abnormality; gastrointestinal ulceration; neuropathy;

XX haematological disease; metabolic disease; sperm dysfunction;

XX thyroid disorder; hypothyroidism; brain damage; colitis;

XX cone photo-transduction deficiency; neurological disease; stroke;

XX trachea; thymus; lymph node; muscular system; obesity; anorexia;

XX growth abnormality; precocious puberty.

XX Homo sapiens.

XX WO200250105-A1.

17-DEC-2001; 2001WO-US049232.

PA
(SMIK) SMITHKLINE BEECHAM CORP.
PA (GLAX) GLAXO GROUP LTD.

N-PSDB; ABQ86170.

Page 313-314; 335pp; English

Sequence 581 AA;

499; Conservative 7: Mismatch

72 PIGSLPFTNPODQGVVAVLGGSPVPVNVLGVPFAAP 65

126 IYAPAHADTGSKL PYI WPEPCGA EKTCS 19.

100

252 HKATMECCUATTHU 245

312 KTKSFTRVVDGAFFPNEPLDLSOKAFKATPSTICINNTTCGGR : 1000

```

: ||| : |||
RDARLACTACUENHNRVTTT 424

```

.....DVGAFVIFIEFKHRPQCFEDTKPAFVKADHADEVRFVFGGAFKGDIVMEGAT 485

45 WTSTIP 550

-2003 (first entry)

therapy; human; secretory protein; membrane proteins; cancer; disease; osteoporosis; tumor

2001; 2001JP-00328381.
2002; 2002ITS-035043EE.

Sugiyama T, Otsuki T, Wakamatsu A, Sato T, Imai T

ADA53168.

SEQ ID NO 2375; 205bp: English

caused by abnormalities of the proteins, e.g., cancer

XX Sequence 525 AA;
 SQ Query Match 84.6%; Score 2606; DB 6; Length 525;
 Best Local Similarity 90.9%; Pred. No. 1.7e-234;
 Matches 501; Conservative 0; Mismatches 0; Indels 50; Gaps 1;

QY 31 GPSAGPQNTRLGWIQKQVTVLSPVNVNVLGVFPAPPLGSLRFTNPQASPMDNL 90
 DB 25 GPSAGPQNTRLGWIQKQVTVLSPVNVNVLGVFPAPPLGSLRFTNPQASPMDNL 84
 QY 91 RRTATYPNICLONSEWLLDQMLKHYKFKGVSEDCLYLNIYAPAHADTGSKLPLYWVF 150
 DB 85 RRTATYPNICLONSEWLLDQMLKHYKFKGVSEDCLYLNIYAPAHADTGSKLPLYWVF 144
 QY 151 PGCAFPTGSASIFDGSALAAEDVLVVVQYRLGIFGFTTWDQAHPGWAKRDQVAALS 210
 DB 145 PGCAFPTGSASIFDGSALAAEDVLVVVQYRLGIFGFTTWDQAHPGWAKRDQVAALS 204
 QY 211 WYQKNIIEFGGDPSSVTIFGESAGAISSVSLILSPMAKGLFKHAKIMESGVAIIPYLEAH 270
 DB 205 WYQKNIIEFGGDPSSVTIFGESAGAISSVSLILSPMAKGLFKHAKIMESGVAIIPYLEAH 264
 QY 271 YKESBDLVVNAHFCGNNASDSBALRCLRTKPSKSLITLSQTKSFTRVVDGAPFNEPL 330
 DB 265 YKESBDLVVNAHFCGNNASDSBALRCLRTKPSKSLITLSQTKSFTRVVDGAPFNEPL 324
 QY 331 DLSQKAFAPISIIIVNNHEGCGFLPMKEAPEILSGSKSLALHLIOMILHIIPQYLT 390
 DB 325 DLSQKAFAPISIIIVNNHEGCGFLPMKEAPEILSGSKSLALHLIOMILHIIPQYLT 384
 QY 391 VANEYFHDGSLTEIRDSLLDLGDFEVVPAALITARYRDGAPVYFYEFRRHPCFED 450
 DB 365 VANEYFHDGSLTEIRDSLLDLGDFEVVPAALITARYRDGAPVYFYEFRRHPCFED 424
 QY 451 TKPAFVKAHDAEVRVFGCAFPLKGDIVNEGATEEEKILSRKMKMYATFARTGNP 510
 DB 425 -----EGATEEEKILSRKMKMYATFARTGNP 454
 QY 511 DLSLPAVNLTEOYLQDILNMSLQRLKEPRVDFMTSTPLILSADMLHSLSLTF 570
 DB 455 DLSLPAVNLTEOYLQDILNMSLQRLKEPRVDFMTSTPLILSADMLHSLSLTF 514
 QY 571 LLOPFFFCAP 581
 DB 515 LLOPFFFCAP 525

RESULT 8
 ABUS4639
 ID ABUS4639 standard; protein; 581 AA.
 XX ABUS4639;
 AC
 XX 03-JUN-2003 (first entry)
 DT
 XX
 DE Human NOVX polypeptide #98.
 XX
 XX Human; NOVX; metabolic disorder; cardiomyopathy; diabetes; ASD;
 KW hypertension; congenital heart defect; aortic stenosis; valve disease;
 KW atrial septal defect; atriocentric canal defect; ductus arteriosus;
 KW pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;
 KW tuberculous sclerosis; scleroderma; atherosclerosis; infectious disease;
 KW obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;
 KW Parkinson's disease; immune disorder; haematopoietic disorder;
 KW haemophilia; hypercoagulation; Crohn's disease; cancer.
 XX
 OS Homo sapiens.
 XX
 PN MO200281498-A2.
 XX
 PD 17-OCT-2002.
 XX

PF 03-APR-2002; 2002MO-US010780.
 XX
 PR 03-APR-2001; 2001US-0281086P.
 PR 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 06-APR-2001; 2001US-0282020P.
 PR 10-APR-2001; 2001US-0282930P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 12-APR-2001; 2001US-0283513P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285381P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0285890P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 25-APR-2001; 2001US-0286292P.
 PR 27-APR-2001; 2001US-0287213P.
 PR 02-MAY-2001; 2001US-0288257P.
 PR 29-MAY-2001; 2001US-0294164P.
 PR 30-MAY-2001; 2001US-0294484P.
 PR 18-JUN-2001; 2001US-0296952P.
 PR 19-JUN-2001; 2001US-0299237P.
 PR 19-JUN-2001; 2001US-0299276P.
 PR 12-SEP-2001; 2001US-0318750P.
 PR 25-SEP-2001; 2001US-0324800P.
 PR 25-SEP-2001; 2001US-0324802P.
 PR 27-SEP-2001; 2001US-0325684P.
 PR 17-OCT-2001; 2001US-0330143P.
 PR 14-NOV-2001; 2001US-0332131P.
 PR 14-NOV-2001; 2001US-0332240P.
 PR 14-NOV-2001; 2001US-0332779P.
 PR 21-NOV-2001; 2001US-0332115P.
 PR 04-DEC-2001; 2001US-0337621P.
 PR 03-JAN-2002; 2002US-0345783P.
 PR 16-JAN-2002; 2002US-0350251P.
 PR 02-APR-2002; 2002US-00114270.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;
 PI Patuturajan M, Liu X, Gusev VY, Li L, Vernet CM, Zehrhusen BD;
 PI Gorman L, Shenoy SG, Pena CE, Smithson G, Burgess CE, Gerlach V;
 PI Padigaru M, Shinkets RA, Gangoli EA, Taupier RJ, Caeman SJ, Ji W;
 PI Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
 PI MacDougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;
 PI Ellerman K;
 XX
 DR WPI: 2003-046858/04.
 DR N-PSDB; ABX72267.
 XX
 PT New isolated NOVX polypeptide useful for treating atherosclerosis,
 PT metabolic disorders, diabetes, obesity, infectious disease, anorexia,
 PT neurodegenerative disorders, Alzheimer's disease and cancer.
 XX
 PS Claim 1; Page 303; 666pp; English.
 XX
 XX The invention relates to human polypeptides, termed NOVX, and the
 CC polynucleotides encoding them. The polypeptides and polynucleotides are
 CC useful for diagnosing disease, and screening for potential therapeutic
 CC agents. The sequences are useful for treating metabolic disorders,
 CC cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic
 CC stenosis, atrial septal defect (ASD), atriocentric canal defect,
 CC ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
 CC septal defect (VSD), valve diseases, tuberculous sclerosis, scleroderma,
 CC atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
 CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
 CC haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
 CC and cancer. Sequences ABUS4542-ABUS4647 represent human NOVX polypeptides
 CC of the invention
 XX

QY 511 DLSLPAVNLTEQYIQLDLMSLGGRLKEPRVDFTSTIP 550
 DB 549 DLSLPAVNLTEQYIQLDLMSLGGRLKEPRVDFTSTIP 588

RESULT 10

ADB64065
 ID ADB64065 standard; protein; 469 AA.

AC ADB64065;

DT 04-DEC-2003 (first entry)

DE Human protein encoded by clone BRAWH20021910.

KM Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
 cell regeneration; membrane protein; signal transduction-related protein;
 transcription-related protein; osteoporosis; neurological disease;
 cancer; tumour.

OS Homo sapiens.

PN EPI308459-A2.

PD 07-MAY-2003.

PF 28-MAR-2002; 2002EP-00007401.

PR 05-NOV-2001; 2001JP-00379298.

PR 25-JAN-2002; 2002US-00350978.

PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isegai T, Sugiyama T, Otsuki T, Makamatsu A, Sato H, Ishii S,
 Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
 Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuko Y;

DR MPI; 2003-450961/43.

DR N-PEDB; ADB62095.

PT New polynucleotides and polypeptides, useful for developing a diagnostic
 marker or medicines for regulation of their expression and activity, or
 as targets of gene therapy.

PS Claim 1; Page; 222pp; English.

CC The invention discloses a polynucleotide comprising a sequence selected
 from 1970 fully defined nucleotide sequences which encode novel

CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 or its partial peptide, an antibody binding to the polypeptide or peptide

CC of the polynucleotide, immunologically assaying the polypeptide or
 peptide of the polynucleotide by contacting the polypeptide or peptide

CC with the antibody of the encoded protein, and observing the binding
 between the two, a transformant carrying the polynucleotide in an

CC expressible manner and an antisense polynucleotide. The oligonucleotide
 is useful as a primer for synthesizing the polynucleotide, or as a probe

CC for detecting the polynucleotide. The polynucleotides and encoded
 proteins are useful as pharmaceutical agents and many disease-related

CC genes may be included in them, for developing a diagnostic marker or
 medicines for regulation of their expression and activity, or as targets

CC of gene therapy. The genes are involved in tissue and/or cell
 regeneration. Membrane proteins, signal transduction-related proteins,

CC transcription-related proteins, disease-related proteins and genes
 encoding them can be used as indicators for diseases (e.g. osteoporosis,

CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
 the activity or expression of the encoded protein to treat diseases. The

CC sequence presented is a protein of the invention. Note: Some of the
 CC sequence data for this patent is not represented in the printed

CC specification, but is based on sequence information supplied by the
 CC European Patent Office.

CC Sequence 469 AA;
 XX 50

Query Match 79.7%; Score 2454; DB 7; Length 469;
 Best Local Similarity 99.6%; Pred. No. 2.4e-220;
 Matches 467; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 113 MLKHYHFFGVSSEDLNINITYAPAHADGSKLPVLVWFGGAFKGSIFDGSALAYE 172
 DB 1 MLKHYHFFGVSSEDLNINITYAPAHADGSKLPVLVWFGGAFKGSIFDGSALAYE 60
 QY 173 DVLVWVVOYRGLIGFQFTTMDQHAPGNMAFPDQVVAALSMVQNIFFGDDSSVTIFGES 232
 DB 61 DVLVWVVOYRGLIGFQFTTMDQHAPGNMAFPDQVVAALSMVQNIFFGDDSSVTIFGES 120
 QY 223 AGAIVSSSLISPMAGKLFHKAIVESGVAIIPYLEAHDIYKESBDLQVVAHFCGNNAADSE 292
 DB 121 AGAIVSSSLISPMAGKLFHKAIVESGVAIIPYLEAHDIYKESBDLQVVAHFCGNNAADSE 180
 QY 223 ALLRCLRTKPSKELLTSQKTSFPRVVDGAFPPHPEPDLISQKAFKAIPISTIGVNNHC 352
 DB 181 ALLRCLRTKPSKELLTSQKTSFPRVVDGAFPPHPEPDLISQKAFKAIPISTIGVNNHC 240
 QY 353 GPLPMKEAPETLISGNSKSLALHLIQLNLIHPQYLHLVANEYFHDKSLTEIRDSLDL 412
 DB 241 GPLPMKEAPETLISGNSKSLALHLIQLNLIHPQYLHLVANEYFHDKSLTEIRDSLDL 300
 QY 413 LGDVFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFYKADHAEVRFVGGAF 472
 DB 301 LGDVFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFYKADHAEVRFVGGAF 360
 QY 473 LKGDIVMEGATEEBEKLISROMKMYWATPARTGNPNNGDLSLMPAYNLTEOYLQDLNMS 532
 DB 361 LKGDIVMEGATEEBEKLISROMKMYWATPARTGNPNNGDLSLMPAYNLTEOYLQDLNMS 420
 QY 533 LGORLKEPRVDFTSTIPLIISASDMLSPSLSTLPLSLQPPFFCAP 581
 DB 421 LGORLKEPRVDFTSTIPLIISASDMLSPSLSTLPLSLQPPFFCAP 469

RESULT 11

ADFS0145
 ID ADFS0145 standard; protein; 542 AA.

AC ADFS0145;

DT 12-FEB-2004 (first entry)

DE Cat cauxin protein SEQ ID NO:2.

KM cat; cauxin; cat kidney disease marker; kidney disease.

OS Felis catus.

PN JP2003250575-A.

PD 09-SEP-2003.

PF 04-MAR-2002; 2002JP-00057908.

PR 04-MAR-2002; 2002JP-00057908.

PA (TOHO-) TOHOKU TECHNOARCH KK.

DR MPI; 2004-002277/01.

DR N-PEDB; ADFS0144.

PT Novel cauxin protein or its salt, useful as a cat kidney disease marker,
 and for diagnosing cat kidney disease.

PS Claim 3; SEQ ID NO 2; 33pp; Japanese.

CC The present sequence represents a cat cauxin protein (I) or its salt,
 CC which is cat kidney disease marker. Also described: (1) a partial peptide
 CC (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector

CC (IV) comprising (III); (4) a transformed host (V) comprising (III) or
 CC (IV); (5) producing (I) or (II) by culturing (V); (6) an antibody (VI)
 CC which couples specifically with (I) or (II); (7) diagnosing cat kidney
 CC disease which involves measuring (I) quantitatively, and where reduction
 CC of amount of (I) indicates presence of the disease; (8) a cat kidney
 CC disease diagnostic agent comprising (I) labelling agent, a reagent which
 CC measures the biological activity of urinary (I) or (VI); and (9) a cauxin
 CC detection kit which measures cauxin in a test sample. (I) is useful as a
 CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney
 CC disease. (I) enables detection of cat kidney disease simply and
 CC correctly. (I) provides an early marker for the disease, and replaces
 CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,
 CC blood testing.

CC Sequence 542 AA;

Query Match 64.5%; Score 1985; DB 8; Length 542;
 Best Local Similarity 71.7%; Pred. No. 2.4e-176;
 Matches 373; Conservative 60; Mismatches 85; Indels 2; Gaps 2;

QY 31 GPSAEGQRNTRIGMIOGKQVTVLGSPPVNVNVLGVFPFAAPLGLSRTNPQASPMNLT 90
 DB 22 GPADABVNRSTRIGWVRGKQTVLGSIVPNMFLGIPVAPPLGLRQKRPALPGNDF 81
 QY 91 REATSYPNLCLQNSEWLLDQHLKVHYPRKGVSEDCLYINITYAPAHADTGSKLPVLWF 150
 DB 82 RNATSYPLCLCFQDLEWLVGYQHVLKVRPKLASBEDCLYINITYAPAHADNGSNLPVWVF 141
 QY 151 PGAFFTGSASIFDGSALAAVEDVLVVVQYRLGIFGFPTTWDQAHAPGNMAFKDQVALS 210
 DB 142 PGAFPMGSASSFDGSALAAVEDVLVITVQYRLGIFGFPTDGHARGNMALLDQVALT 201
 QY 211 WQKNIEFGDPSVTVTFGESAGAISSVSLISPMAGLPHKAIMESGVAIIPTL-EAH 269
 DB 202 WVRDNIIEFGDPSVTVTFGESAGAISSVSLISPIANGLPHKAIMESGVAIIPLMRPP 261
 QY 270 DYKESDDQVYAHFPGNNADESEALRLRTPKSKELLTLOKTSFTRVVDGAFPPNRP 329
 DB 262 GDERKDDQVYARICGHASDASALLQCLRAKPESELMDSKLTSPIDDPFFDEE 321
 QY 330 LDLSQKAFKAIPSTIIGVNNHECGFLPMKEAPBIIISGNSKSLALHLIONLHIIPQYLH 389
 DB 322 VALLTQKAFNSVPSIIIGVNNHECAFLL-STFSEIILGGSNRSALALVHTPLNIPQYLH 380
 QY 390 LVANEYFHDKSLTEIRDSLLDLGDVFFVVPALITARYHRDAGAPVYFEFRHRPQCE 449
 DB 381 LVADHYFYNKHSPEIRDSFLDLGDVLFVVPGVYARHRDAGAVYFEFRHPQCLN 440
 QY 450 DTKPAFYKADHAEVRFVFGAFLKGDIVFEGATEEBEKLRSKMKYATARTGNPN 509
 DB 441 DTRPAFYKADHSDIRVFGAFLKGDIVFEGATEEBEKLRSKMKRYANFARTGDPNG 500
 QY 510 NDLSMPAYNLTEQYLODLNMSLGRLKEPRVDFTSTI 549
 DB 501 EGVPLMPAYNQSEQYKLTLDSVSVGQKLXEOVEIFPMNTI 540

RESULT 12
 ADF50147
 ID ADF50147 strand; protein; 542 AA.
 AC ADF50147;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Cat cauxin protein SEQ ID NO:4.
 XX
 KM cat; cauxin; cat kidney disease marker; kidney disease.
 XX
 OS Felis catus.
 XX
 FN JP2003250575-A.
 XX

PD 09-SEP-2003.
 XX
 PF 04-MAR-2002; 2002JP-00057908.
 XX
 PR 04-MAR-2002; 2002JP-00057908.
 XX
 PA (TOHO-) TOHOKU TECHNOARCH KK.
 XX
 DR WPI; 2004-002277/01.
 DR N-PDB; ADF50146.
 PT Novel cauxin protein or its salt, useful as a cat kidney disease marker,
 FT and for diagnosing cat kidney disease.
 PS Disclosure; SEQ ID NO 4; 33pp; Japanese.

The present sequence represents a cat cauxin protein (I) or its salt,
 CC which is cat kidney disease marker. Also described: (1) a partial peptide
 CC (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector
 CC (IV) comprising (III); (4) a transformed host (V) comprising (III) or
 CC (IV); (5) producing (I) or (II) by culturing (V); (6) an antibody (VI)
 CC which couples specifically with (I) or (II); (7) diagnosing cat kidney
 CC disease which involves measuring (I) quantitatively, and where reduction
 CC of amount of (I) indicates presence of the disease; (8) a cat kidney
 CC disease diagnostic agent comprising (I) labelling agent, a reagent which
 CC measures the biological activity of urinary (I) or (VI); and (9) a cauxin
 CC detection kit which measures cauxin in a test sample. (I) is useful as a
 CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney
 CC disease. (I) enables detection of cat kidney disease simply and
 CC correctly. (I) provides an early marker for the disease, and replaces
 CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,
 CC blood testing.

Sequence 542 AA;

Query Match 64.5%; Score 1985; DB 8; Length 542;
 Best Local Similarity 71.7%; Pred. No. 2.4e-176;
 Matches 373; Conservative 60; Mismatches 85; Indels 2; Gaps 2;

QY 31 GPSAEGQRNTRIGMIOGKQVTVLGSPPVNVNVLGVFPFAAPLGLSRTNPQASPMNLT 90
 DB 22 GPADABVNRSTRIGWVRGKQTVLGSIVPNMFLGIPVAPPLGLRQKRPALPGNDF 81
 QY 91 REATSYPNLCLQNSEWLLDQHLKVHYPRKGVSEDCLYINITYAPAHADTGSKLPVLWF 150
 DB 82 RNATSYPLCLCFQDLEWLVGYQHVLKVRPKLASBEDCLYINITYAPAHADNGSNLPVWVF 141
 QY 151 PGAFFTGSASIFDGSALAAVEDVLVVVQYRLGIFGFPTTWDQAHAPGNMAFKDQVALS 210
 DB 142 PGAFPMGSASSFDGSALAAVEDVLVITVQYRLGIFGFPTDGHARGNMALLDQVALT 201
 QY 211 WQKNIEFGDPSVTVTFGESAGAISSVSLISPMAGLPHKAIMESGVAIIPTL-EAH 269
 DB 202 WVRDNIIEFGDPSVTVTFGESAGAISSVSLISPIANGLPHKAIMESGVAIIPLMRPP 261
 QY 270 DYKESDDQVYAHFPGNNADESEALRLRTPKSKELLTLOKTSFTRVVDGAFPPNRP 329
 DB 262 GDERKDDQVYARICGHASDASALLQCLRAKPESELMDSKLTSPIDDPFFDEE 321
 QY 330 LDLSQKAFKAIPSTIIGVNNHECGFLPMKEAPBIIISGNSKSLALHLIONLHIIPQYLH 389
 DB 322 VALLTQKAFNSVPSIIIGVNNHECAFLL-STFSEIILGGSNRSALALVHTPLNIPQYLH 380
 QY 390 LVANEYFHDKSLTEIRDSLLDLGDVFFVVPALITARYHRDAGAPVYFEFRHRPQCE 449
 DB 381 LVADHYFYNKHSPEIRDSFLDLGDVLFVVPGVYARHRDAGAVYFEFRHPQCLN 440
 QY 450 DTKPAFYKADHAEVRFVFGAFLKGDIVFEGATEEBEKLRSKMKYATARTGNPN 509
 DB 441 DTRPAFYKADHSDIRVFGAFLKGDIVFEGATEEBEKLRSKMKRYANFARTGDPNG 500
 QY 510 NDLSMPAYNLTEQYLODLNMSLGRLKEPRVDFTSTI 549

Db 501 EGVPLMPAYTQSEQYLKLDLSVWGQKKEQVEFMNNTI 540

RESULT 13

ABP61006 ID ABP61006 standard; protein; 356 AA.

XX AC ABP61006;

DT 10-SEP-2002 (first entry)

XX DE Novel human protein. SEQ ID 93.

XX Human; cytosolic; vulnary; antiarteriosclerotic; antiparkinsonian;
XX neurotropic; neuroprotective; immunosuppressive; haemostatic;
XX antiinflammatory; cardiac; antitumor; virucide; antithyroid;
XX cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
XX wound healing disorder; atherosclerosis; Parkinson's disease;
XX Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
XX inflammation; neoplastic disease; nervous system disorder;
XX cardiovascular disorders; pancreatic; respiratory disorder;
XX hyperproliferation; systemic autoimmune disease; hyper-immunity;
XX developmental abnormality; gastrointestinal ulceration; neuropathy;
XX haematological disease; metabolic disease; sperm dysfunction;
XX thyroid disorder; hypothyroidism; brain damage; colitis;
XX cone photo- transduction deficiency; neurological disease; stroke;
XX angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
XX trachea; thymus; lymph node; muscular system; obesity; anorexia;
XX growth abnormality; precocious puberty.

XX Homo sapiens.

XX WO200250105-A1.

XX PD 27-JUN-2002.

XX PF 17-DEC-2001; 2001WO-US049232.

XX PR 19-DEC-2000; 2000US-0256710P.

XX PR 20-DEC-2000; 2000US-0257048P.

XX PR 09-JAN-2001; 2001US-0260482P.

XX PR 30-JAN-2001; 2001US-0264922P.

XX PR 06-FEB-2001; 2001US-0266797P.

XX PR 19-MAR-2001; 2001US-0276988P.

XX PR 04-APR-2001; 2001US-0281535P.

XX PR 08-MAY-2001; 2001US-0289622P.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PA (SMIK) SMITHKLINE BEECHAM PLC.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Agarwal P, Birkeland M, Cogswell JP, Kahnick KF, Lai Y;

XX PI Mathensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;

XX DR WPI: 2002-508784/54.

XX DR N-PSDB, ABQ86171.

XX PT Secreted proteins and polynucleotides useful as vaccines for preventing

XX PT or treating various diseases e.g. cancer, wounds, atherosclerosis,

XX PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.

XX PS Claim 1(a); Page 315; 335pp; English.

XX The invention relates to an isolated polypeptide with signal sequences

XX which allow it to be secreted extracellularly or membrane associated. The

XX activity of polypeptides of the invention may be described as,

XX cytosolic, vulnary, antiarteriosclerotic, antiparkinsonian, neurotropic,

XX neuroprotective, immunosuppressive, haemostatic, antiinflammatory,

XX cardiac, antitumor, virucide, antithyroid, cerebroprotective, anorectic,

XX and metabolic. Polypeptides and polynucleotides of the invention are

XX useful in the treatment, or as a vaccine in the prevention of, cancer,

XX wound healing disorders, infection, atherosclerosis, Parkinson's disease

XX and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,

CC inflammation, neoplastic diseases, nervous system related disorders and
CC cardiovascular disorders, pancreatitis, respiratory disorder,
CC hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC developmental abnormality, gastrointestinal ulceration, neuropathy,
CC haematological diseases, metabolic diseases, sperm dysfunction, thyroid
CC disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC transduction deficiency, neurological diseases, stroke, angiogenesis,
CC ovulation disorder, diseases in the spinal cord, thyroid gland, heart,
CC trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC growth abnormalities, and alleviation of precocious puberty. The
CC sequences given in record ABP60965-ABP61019 represent novel human
CC proteins of the invention

XX SQ Sequence 356 AA;

Query Match 57.8%; Score 1780; DB 5; Length 356;
Best Local Similarity 100.0%; Pred. No. 2e-157;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 ILSPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAHFCGNASDSEALLRCURTQ 301

Db 17 ILSPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAHFCGNASDSEALLRCURTQ 76

QY 302 PSKELLTSLQKTSFTRVVDGAFPPNPDLDSQAKAIPSIIGVNNHCGFLLPMKEA 361

Db 77 PSKELLTSLQKTSFTRVVDGAFPPNPDLDSQAKAIPSIIGVNNHCGFLLPMKEA 136

QY 362 PEILSGNSKSLALHLINILHIPPQYHLVANEYFHDKSLTEIRDSLDDLGDVFFVVP 421

Db 137 PEILSGNSKSLALHLINILHIPPQYHLVANEYFHDKSLTEIRDSLDDLGDVFFVVP 196

QY 422 ALITARYHDAAGAVVEYEFRRHRPQCFEDTKPAFVKADHADVAFVGAFLLKGDIVME 481

Db 197 ALITARYHDAAGAVVEYEFRRHRPQCFEDTKPAFVKADHADVAFVGAFLLKGDIVME 256

QY 482 GATEEEKLISRKMKKYATARTGNPNNDLSLMPAYNLTEQYLQDLNLSLGGRLKEPR 541

Db 257 GATEEEKLISRKMKKYATARTGNPNNDLSLMPAYNLTEQYLQDLNLSLGGRLKEPR 316

QY 542 VDFWSTIPLILASDMLHSPLSLTFSLLOPPFFCAP 581

Db 317 VDFWSTIPLILASDMLHSPLSLTFSLLOPPFFCAP 356

RESULT 14

AAE20911 ID AAE20911 standard; protein; 561 AA.

XX AC AAE20911;

XX DT 01-JUL-2002 (first entry)

XX DB Rat carboxylesterase-like enzyme protein.

XX KW Rat; carboxylesterase-like enzyme; organophosphorus intoxication;

XX KW osteopathic; gene therapy; osteoporosis; antisense therapy; cytosolic;

XX KW detoxifying agent; Paget's disease; bone implant degradation; cancer;

XX KW dental implant; enzyme; gene expression.

XX OS Rattus sp.

XX PN WO200206454-A2.

XX PD 24-JAN-2002.

XX PF 10-JUL-2001; 2001WO-EP007919.

XX PR 17-JUL-2000; 2000US-0218564P.

XX PA (FARB) BAYER AG.

XX PI Xiao Y;


```
Db      16  GODSASPIRTHTGQVLSLVHVKGANAGVOTFLGIPPAKPPGLRPAPEPPESWGV 75
Qy      91  REATSYPNLCTON-----SEWLLDQMLKVHYPKFVSEBDLYNITYAPAHADGSKLP 145
Db      76  RDGTHPAMCQDLTAVERSEFL-----SQPNMTFSDSMSBDCLYSTITPAHSHGSHLP 131
Qy      146 VLWVFPFGAFKTSASIFDGSALAAVEDVLVVVVQYRLGIFGFTTWQDHAFGNAFKDQ 205
Db      132 VMVVIHGALVFGMASLYDGSWLALENVVVVIQYRLGVLGFFSTGDKHATGNWGYLDQ 191
Qy      206 VVALSTWQKNIIEFPGDSSVTIIFESAGAISVSSLISPMAGLPHKAIMESGVAIIPY 265
Db      192 VVALRWQONIAHFGGNPDRVTIIFESAGTSVSSLVSPISQGLFHGAIMESGVALLPG 251
Qy      266 LEADYEKSEDL--QVVAHFCGNNASDSEALLRCLRTKPSKELTLSQKTSFTRVNDGA 323
Db      252 LIA-----SSADVISTVVANLACDQVDSBALVGCURGKSKERIILANKPFIKIPGVVDGV 307
Qy      324 FFPNEPLDLSQAKFKALPSIIGVNNHECGFLP---MKAPEILSGSNKSLALHLIQN 379
Db      308 FLPRHPQELASADRPVPSIVGVNNNEFGWLIIPKWRIVDTQKEMDREASQALQKMLT 367
Qy      380 ILHIPPQYLHVANEFYFDKXSLTEIRDSLDDLGDVFPVVPALITARYHRDAGAPVYFY 439
Db      368 LLMLEPTFGDLIREEYIGDNGDPQTLQAFQEMMADSMFVIPALQVAHF-QCSRAPVYFY 426
Qy      440 EFRHRPQCFEDTKPAFVADHADEVRFVFGGAFLLKGDIVMEGATEEEKLSRKKMKYMA 499
Db      427 EFQHPKSWLKNIRPPHMKADHGDLPFVF-RSFFGANYIKF--TEEEQLSRKKMKYMA 482
Qy      500 TFARTGNPENGNDLSIMPAYNLTEQYLQDLNMSLQORLKEPRVDFWTSTIP 550
Db      483 NFAIRNGNPNRGSLPHWPLFDQEBQYLQNLQPAVGRAKKAHRLQFWKCALP 533
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Search completed: June 16, 2005, 20:41:52
Job time : 173 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 16, 2005, 20:28:44 ; Search time 43 Seconds
(without alignments)
1300.045 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 3079
Sequence: 1 MPOGLTSSASQWCFLLIQP.....PLSLRFLSLQPFPPFCAP 581

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1298.5	42.2	557	2	A47162 thiolesterase B (B
2	1231.5	40.0	532	2	A34329 60K esterase (EC 3
3	1230	39.9	559	1	UC5408 carboxylesterase (
4	1199	38.9	561	2	847655 carboxylesterase (
5	1186.5	38.5	554	1	834607 carboxylesterase (
6	1163	37.8	554	2	A39060 carboxylesterase (
7	1162.5	37.8	566	2	819307 carboxylesterase (
8	1144	37.2	549	2	UK0054 carboxylesterase (
9	1140	37.0	567	1	A41010 carboxylesterase (
10	1139	37.0	561	2	862788 carboxylesterase (
11	1138.5	37.0	562	2	A55281 carboxylesterase (
12	1136	36.9	540	2	A31584 carboxylesterase (
13	1129.5	36.7	561	2	571597 carboxylesterase (
14	1123	36.5	561	2	UC2447 carboxylesterase (
15	1121.5	36.4	565	2	810367 carboxylesterase (
16	1034.5	33.6	539	2	A29923 carboxylesterase (
17	777	25.2	596	1	ACRYE acetylcholinestera
18	764.5	24.8	614	2	A39256 acetylcholinestera
19	763	24.8	614	2	UH0314 acetylcholinestera
20	756	24.6	599	1	A38868 acetylcholinestera
21	754	24.5	614	2	ACHU acetylcholinestera
22	752	24.4	602	1	ACHU acetylcholinestera
23	740	24.0	603	2	870849 cholinesterase (EC
24	732	23.8	581	2	C39768 cholinesterase (EC
25	726.5	23.6	584	2	848724 acetylcholinestera
26	710.5	23.1	583	2	810712 acetylcholinestera
27	692.5	22.5	620	2	AS4413 acetylcholinestera
28	660	21.4	745	2	813586 triacylglycerol 11
29	658.5	21.4	489	2	B69680 para-nitrobenzyl e

30	643.5	20.9	597	2	A33668 sterol esterase (E
31	633.5	20.6	599	2	A57701 sterol esterase (E
32	627.5	20.4	664	2	JC7990 acetylcholinestera
33	618	20.1	612	2	A34967 sterol esterase (B
34	594.5	19.3	691	2	JB0150 acetylcholinestera
35	593	19.3	550	1	A34576 crystal protein pr
36	586	19.0	767	2	847639 acetylcholinestera
37	581.5	18.9	746	2	A25363 acetylcholinestera
38	575	18.7	540	2	551043 carboxylesterase (
39	572.5	18.6	602	2	T37254 acetylcholinestera
40	570.5	18.5	637	2	866236 acetylcholinestera
41	569.5	18.5	554	2	T31783 hypothetical prote
42	569.5	18.5	557	2	A56690 esterase - Caenorh
43	562.5	18.3	545	2	A89046 sterol B0238.1 (1
44	557.5	18.1	593	1	825062 triacylglycerol 11
45	551	17.9	562	2	827782 esterase precursor

ALIGNMENTS

RESULT 1

thiolesterase B (EC 3.-.-.-) precursor - mallard
C/Species: Anas platyrhynchos (mallard)
C/Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 09-Jul-2004
C/Accession: A47162
R/Hwang, C.S.; Koliatukudy, P.E.
J. Biol. Chem. 268, 14278-14284, 1993
A/Title: Molecular cloning and sequencing of thioesterase B cDNA and stimulation of expt
A/Reference number: A47162; MUID:93300823; PMID:8314791
A/Accession: A47162
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-557 <HMA>
A/Cross-References: UNIPROT: Q04791; GB: L05493; NID: g213100; PIDD: AAA49223.1; PIDD: g213101
A/Superfamily: cholinesterase; cholinesterase homology
C/Keywords: hydrolase
F/56-545/Domain: cholinesterase homology <CHE>

Query Match	42.2%	Score 1298.5	DB 2	Length 557
Best Local Similarity	48.4%	Pred. No. 4.1e-94		
Matches 265	Conservative 177	Mismatches 177	Indels 27	Gaps 8
QY	30	TGSAEGPQNTTRGWIQKQVTVLGSPPVNVFLGVFAAPPLGSLRFTNPQSPMDN	89	
DB	23	TGQAEQPEVYVNTNGSVRGYQVKNABRSVNVFLGPAKPPVGPFRFSRQPPERPKG	82	
QY	90	LRBATSYPNLCIQNSEWILLDOHML-----KVHYPKFVSEDCLYNIYAPAHADTGSKL	144	
DB	83	VRDAASYPMCLQDK---VLGQYLSDAITNRKEKVRRLQISDCLYNVYTVSTBEDKTL	139	
QY	145	PVLVWPFPGAFKTSASIFDGSALAYEDVLVVVQVRLGIFGFTTWDQAPGNMAFKD	204	
DB	140	PVFVWINGGGLVSGAASVYGSALAFDNNVVYTIQRLGAGYFSGDCKARLNMGULD	199	
QY	205	QVALSWQKNIRFPFGDPSVTFEGSAGAVSSVLSLSPMAKGLPHKAIMESGVAL-I	263	
DB	200	QVALQWIOENTIHFRDPSGVTFEGSAGVSVSLVLSPLAKGLHKAISEGTVARI	259	
QY	264	PYLEAHVYKSESDIQVVAHFCGNNAUSDSEALLRLCTRPSKET--LTLISQTKSPTRVVD	321	
DB	260	LFTB-----QPEBQQRILAAAGCKSSSALLVECLARKTEAMEQWQITLKMPMPWISASLD	315	
QY	322	GAFFPNEPLDLSQAKFALPSITIGVNNHCGFLIP-MKEAPELSSNKSALHLIONT	380	
DB	316	GVFPKSPQRLSKRVNAPVYIIGVNNCEGWTLPMMKFPETBELKDVAVQVLOST	375	
QY	381	LHI-----PPQYHLVANEYFHDKHSLTBRDSLLDGLGVFVFPVPLITARYRDGAP	435	
DB	376	LALFKGAPSDIVLVVNEIYIYVNAENRAQVRDGLDIDAPLIPFVSAYEVARHHRDGNP	435	
QY	436	VYFYEFRHRPQCFEDTRPAFVKADHADEVRFVFGAFLKGDIVMFEGATEBEKLLSRKM	495	

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Db      436 VYFEFQHRPSSAGVPEFVKADHDELAIFVGFAPLAGN-----ATEEBAKLSRTVM 489
QY      496 KYWATFAPATGNPNDLSLWPAVNLTEOYLQDLNMSIGORLKEPRVDFTSTIPLILSA 555
Db      490 KYWNTNARKNGPNBGLVHWPQYDMDERYLEIDLQKAAKKLKERKQKFFMWQLTEQIMSD 549
QY      556 SDMWHSPL 563
Db      550 RRRKHTDL 557

RESULT 2
A34329
60K esterase (EC 3.1.1.-) isoform 2 - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C/Accession: A34329
R102019, J.
J. Biol. Chem. 264, 12533-12545, 1989
A/Title: Isolation, properties, and the complete amino acid sequence of a second form of
A/Accession: A34329; MUID:89308686; PMID:2745458
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-532 <OZO>
A/Cross-references: UNIPROT:P14943
C/Superfamily: cholinesterase, cholinesterase homology
C/Keywords: carboxylic ester hydrolase
F/33-517/Domain: cholinesterase homology <CHE>
F/201,430/Active site: Ser, His #status predicted

Query Match      40.0%; Score 1231.5; DB 2; Length 532;
Best Local Similarity 47.8%; Pred. No. 7,2e-89;
Matches 253; Conservative 76; Mismatches 167; Indels 33; Gaps 7;

QY      37 PQRNRLGMIQOKOYTVLGSVPVNVFLGVPPAAPPLGSLRFTNPOPASPMNDLREKTSY 96
Db      6 PQRNHTGQVRSLVHVEGTDAVHTFLGIPAKPRLGRLFAPRPAEAMSGVRDSTL 65
QY      97 PNLCLQNSBMLLDQMLKVVH--PKFGVSEDCIYNIYAPAHADTGSKLPLVWPFGQA 154
Db      66 PAMCLQN--LAIMQDVLLHFTPPSLPMSSEDCIYNIYAPAHARESDLPVWVWTHGG 123
QY      155 FRTSGAIFDGSALAAVEDLVVVVQYRLGIFGFTTMDHAPGNMAFKQVVALSMWOK 214
Db      124 LTMGASMYDSSALAAFEDEVVVTIYQRLGVLFSTGDAHNGNGYLDQVAAALRWOK 183
QY      215 NIEFFGDPSSVTIFGSSAGAISVSSLLSPMAKGLFHKAIMESGVAIIPLYEADHYEKS 274
Db      184 NIAHFGNPRGVITIFGSSAGTSVSHVLSFMSQGLFHGAIMESVALLPGLITSSSEVY 243
QY      275 EDLOVAHFGGNNADESEALLRCLRTKPSKELLTTSQTKTSFTRVYDGAFFNEBLDLS 334
Db      244 S--TVVANSLSRCQGVSELTVLRCLRAKSEBMLAIQVFMILPGVVDVFLPRHPEELLA 301
QY      335 QKAFKAIPIISIIIVNNHECGFLP-----MKEAPIISGNSKSLALHLIQNIL 381
Db      302 LADFQVPSIIGINDEYEWIIPKLLAIDPOEEDRDQAMREIMQATKQLML----- 354
QY      382 HIIPQYLHVAVEYFDKSLTEIRDSLDLDLGDVFFVPPALITRARIYRDAGAVTYFER 441
Db      355 --PPALGDLIMDEYNSNEDPKHLMAQFQEMWADMFMFPAIRYAHQOR-SHAFTYFER 411
QY      442 RHRPQCFEDTKPAFYKADHADVRFVFGAFLKGDIVFBGATEEKKLSRKMKYWA 501
Db      412 QRPSFTKDLRPHRAHGDGVVFFVFSHLFGSKVPL---TEEFELSRRWKWTANP 467
QY      502 ARTGPNNGNDLSLWPAVNLTEOYLQDLNMSIGORLKEPRVDFTSTIIP 550
Db      468 ANNRPNBEGLAHWPLFDLQRYLQNNQPAVGALAKRRLQRFHTHTLP 516

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RESULT 3
JC5408
carboxylesterase (EC 3.1.1.1) - human
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: JC5408
R/Schwer, H.; Langmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, G.
Biochem. Biophys. Res. Commun. 233, 117-120, 1997
A/Title: Molecular cloning and characterization of a novel putative carboxylesterase, pte
A/Reference number: JC5408; MUID:97289502; PMID:9144407
A/Accession: JC5408
A/Molecule type: mRNA
A/Residues: 1-559 <SCH>
A/Cross-references: UNIPROT:O00748; GB:Y09616; NID:92058317; PIDN:CAA70831.1; PID:9205831
A/Experimental source: intestine
C/Comment: This enzyme hydrolyzes many xenobiotics, such as carboxyl esters, chloesters &
C/Genetics:
A/Gene: GDB:CE82; ICE; CE2
A/Cross-references: GDB:9959011
C/Superfamily: cholinesterase; cholinesterase homology
C/Keywords: carboxylic ester hydrolase; glycoprotein
F/58-544/Domain: cholinesterase homology <CHE>
F/15-95,123-280,291-428/Disulfide bonds: #status predicted
F/11,276/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/228,457/Active site: Ser, His #status predicted

Query Match      39.9%; Score 1230; DB 1; Length 559;
Best Local Similarity 46.7%; Pred. No. 1e-88;
Matches 248; Conservative 91; Mismatches 168; Indels 24; Gaps 8;

QY      31 GPSAEGPQRNRLGMIQOKOYTVLGSVPVNVFLGVPPAAPPLGSLRFTNPOPASPMNDL 90
Db      26 GQDASPLRTHTHQVGLSVHVGANAVQYQTLGIPAKPRLGRLFAPRPAEAMSGVRS 85
QY      91 REATSPNLCLQN-----SEMLLDQMLKVVH--PKFGVSEDCIYNIYAPAHADTGSKLPL 145
Db      86 RDGTTHPMCLQDLTAVESFPL-----SQFNWTFPSSDSEDCIYNIYAPAHARESDLPV 141
QY      146 VLVWFPFGAKTKTSASIFDGSALAAVEDLVVVVQYRLGIFGFTTMDHAPGNMAFKQV 205
Db      142 VMWVTHHGALVFPGMASLYGSMALLENVWVVIYQRLGVLFSTGDKAHATGMWGYDQ 201
QY      206 VVALSMWQKNIIEFGSDPSSVTIFGSSAGAISVSSLLSPMAKGLFHKAIMESGVAIIPLY 265
Db      202 VVALRWQGNIAHFGNPNRVTIIFGSSAGTSVSSLVVPSISQGLFHGAIMESGVALLPG 261
QY      266 LEADHYEKSDEL--QVVAHFGGNNADESEALLRCLRTKPSKELLTTSQTKTSFTRVYDGA 323
Db      262 LIA---SSADVIISTVIVANLSACDQVDSEALVGCIRGSKSEILAIYKPRMILPGVVDG 317
QY      324 FFPNEPLDLSQKAFKAIPIISIIIVNNHECGFLP-----MKEAPIISGNSKSLALHLIQ 379
Db      318 FLPRHQBELMASADQAPPSIVGNNNEFGWLIPKWRIVDTQKEMDREASQAALQKMLT 377
QY      380 IHIIPQYLHVAVEYFDKSLTEIRDSLDLDLGDVFFVPPALITRARIYRDAGAVTYFER 439
Db      378 LMLRPFTGDLIREBYIGDNGDPQTLQAQFQEMWADMFMFPAIRYAHQOR-QCSRADVYF 436
QY      440 EFRHRPQCFEDTKPAFYKADHADVRFVFGAFLKGDIVFBGATEEKKLSRKMKYWA 499
Db      437 EFGHQPSMLKXIRPAPHKAHGDDELPRV-RSFFGNVYIKF--TEEFQLSRKMKYWA 492
QY      500 TPAATGPNNGNDLSLWPAVNLTEOYLQDLNMSIGORLKEPRVDFTSTIIP 550
Db      493 NFAANGPNBEGSLPHWPLFDQEOYQLNQLPRAVGALAKRRLQRFHTHTLP 543

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RESULT 4
S47655
carboxylesterase (EC 3.1.1.1) precursor - golden hamster
C/Species: Mesocricetus auratus (golden hamster)
C/Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C/Accession: S47655

```

R:Stone, T.; Isobe, M.; Takabatake, E.; Wang, C.Y.
 Biochim. Biophys. Acta 1207, 138-142, 1994
 A:Title: Cloning and sequence analysis of a hamster liver cDNA encoding a novel putative
 A:Reference number: 547655; MUID:94318665; PMID:8043605
 A:Accession: 547655
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-561 <SON>
 A:Cross-references: UNIPROT:064419; EMBL:D28566; NID:9531238; PIDN:BA05913.1; PID:95312
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase
 F:58-546/Domain: cholinesterase homology <CHE>
 F:227,459/Active site: Ser, His #status predicted

Query Match 38.9%; Score 1199; DB 2; Length 561;
 Best Local Similarity 47.3%; Pred. No. 2,8-86;
 Matches 252; Conservative 74; Mismatches 181; Indels 26; Gaps 7;

QY 31 GPSAEGPQNRTRLGWIOGKQVTVLGSPPVNVNVLGVPAPAPLGLRFTNPQASPMNDL 90
 DB 26 GDSVSPIRNTHTGQVGRGLVYKGVYGVYAFGLIPPAKPPVGLRPAPEPPEPMGCV 85
 QY 91 REATSPYMLCQNSWMLLDQHLKVNHPKGVSEDCIYNITVAAHADTGSKLPLVWF 150
 DB 86 RDGTEPAMCLOTDFMRPQISKERKIIIPITSMSEDCIYNITVPAHAHSGSNLFWMWI 145
 QY 151 PGAFKTSASIFDGSALAAVEDLVVVVQYRLGIFGFTTWDQAPGNMAFKDOVALS 210
 DB 146 HGGALVWGMASNDSSLLAATEDIYVSIQYRLGLGFFSTGDEHARGNMGILDVALH 205
 QY 211 WVOXNIEFFGGDPSSVTIFGESAGAIVSLSLISPMAGLPHKAIMESGVALIPYLEAD 270
 DB 206 WYQONIAFFGNGPQGVTFYGVSAAGTSVSLVSPMSKGLFGALMGQVALLPDL-1SD 264
 QY 271 YEKSEDLQVNAHFCNNASDSFALLRCLETPKSKLLTLISQTKTSFTRVYDCAFPENBL 330
 DB 265 TPBAVYTVVNVANQSCSEAKDSFALVHCLEKTEABIIAINOVFIPTPGVVDIFLPRHQ 324
 QY 331 DLISQAKFALPSIIGVNNHECGFLPM-----KEAPEILSGNKSLLALHILQIL 381
 DB 335 ELLASVDHNPVPSIIGVSDCEGMGVPFLFMGLDHVYIKVITRETLPAFLKSRAHMM---- 380
 QY 382 HIRPOLHIVANEFYHDKHSLTEIRDSLILDLGDFVFPVVALITARYHRDAGAPVYEF 441
 DB 381 -LPEPCSLLMQGVMDVBDPOTLQAQFRELKMDPMFVLPALKAVYFQR-SHAPVYFEEF 438
 QY 442 RHRPQCF--EDTKPAFVADHADEVRFVPGAF--LKGDIVMEGATEBEKLSRKMKY 497
 DB 439 QHQSFFIKKDKARPAHVADHDHVAFFVGSDFMGLKIDL-----TEBEKLLNRRMKY 492
 QY 498 WATFARTGNPNNDLSLMPAVYLTBOYLQDLNMSLQGLKEPRVDFTSTIP 550
 DB 493 WANFRRHGNPNSGLPYWPELVHDQYKLDIQPAVGALSKRKLHFWTKLP 545

RESULT 5
 S34607
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: S34607
 R:Aida, K.; Moore, R.; Negishi, M.
 Biochim. Biophys. Acta 1174, 72-74, 1993
 A:Title: Cloning and nucleotide sequence of a novel, male-predominant carboxylesterase
 A:Reference number: S34607; MUID:9332638; PMID:7916639
 A:Accession: S34607
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-554 <AID>
 A:Cross-references: UNIPROT:063880; GB:S64130; NID:9404388; PIDN:AA827606.1; PID:9404388
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase
 F:46-536/Domain: cholinesterase homology <CHE>

F:215,443/Active site: Ser, His #status predicted

Query Match 38.5%; Score 1186.5; DB 1; Length 554;
 Best Local Similarity 46.5%; Pred. No. 2,7-85;
 Matches 256; Conservative 81; Mismatches 183; Indels 31; Gaps 10;

QY 13 CFFILLOPLGHRMGKTGPSAEGPQNRTRLGWIOGKQVTVLGSPPVNVNVLGVPAPAPL 72
 DB 3 CILLIIFPTTV-----IGPVCTQPEVDYTPGRRGRQVGVKQDIDRMNVNVLGIPIFAQAP 55
 QY 73 LGSRLTNPOASPMDNREATSPYMLCQNSWMLLDQHLKVNHPKGVSEDCIYNIT 132
 DB 56 LGPLRFSAPLDPQWEGVRDASINPMLCQDVERMSNRFLNEMKIFPISSECLTINI 115
 QY 133 YAPAHADTGSKLPLVWFPGGAFKTSASIFDGSALAAVEDLVVVVQYRLGIFGFTTW 192
 DB 116 YSPFETITAGDRPVMWVHGGSLRVGSGTSHDGSALAAVGVVVVQYRLGIFGLSTG 175
 QY 193 DQAPGNMAFKDOVALSVOXNIEFFGGDPSSVTIFGESAGAIVSLSLISPMAGLPH 252
 DB 176 DKHMPGNRGLDVVAALRWQGNLAPGCDPNCVTIFGNSAGIIVSLSLSPMSAGLPH 235
 QY 253 KAIMESGVALIPYLEADHYEKSEDLQVNAH--FCGNNASDSEALLRCLETPKSKELLTL 310
 DB 236 RAISQSGVJISKILE--DLNAMESAQNPAHSVACG-SASPAE-LVQCLLQKGGDLITKK 291
 QY 311 QKTSFTRVYDCAFPENBLDLSQAKFALPSIIGVNNHECGFL-----PMKE-A 361
 DB 292 NVNISYLT--VNDSEFPQRPQKLLNKPFPYVILGYTNHFGWLLKFNWILDKMELHS 349
 QY 362 PELISGNSKSLALHILQNLHIIPPOLHIVANEFYHDKHSLTEIRDSLILDLGDFVFP 421
 DB 350 QEDILNRSPLAH-----MQLPEIMPVTIDEVLNDSDESARVYALQELGLDITVLP 404
 QY 422 ALIARHRDGAIVYFEFRHRPQCFEDTKPAFVADHADEVRFVPGAF--KGDIVM 479
 DB 405 TLISFKYLDGCEVPFLYEFQHTSSFAKFPAAVKAHDHSENAFVREGPFLTPBESSILA 464
 QY 480 FEGATEBEKLSRKMKYMAFARTGNPNNDLSLMPAVYLTBOYLQDLNMSLQGLKE 539
 DB 465 FPEATEBEKQSLTMMQMSQFARTGNPNKGKLPWQQLNDEQLYELIGLPRRGVTLKK 524
 QY 540 PRVDFWTSTIP 550
 DB 525 GRLOFWTETLP 535

RESULT 6
 A39060
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 09-Jul-2004
 C:Accession: A39060
 R:Ovnic, M.; Tepperman, K.; Medda, S.; Elliott, R.W.; Stephenson, D.A.; Grant, S.G.; Gane
 Genomics 9, 344-354, 1991
 A:Title: Characterization of a murine cDNA encoding a member of the carboxylesterase mult
 A:Reference number: A39060; MUID:91169540; PMID:1840565
 A:Accession: A39060
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-554 <OVN>
 A:Cross-references: UNIPROT:P23953; GB:M57960; NID:9192853; PIDN:AAA63297.1; PID:9192854
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase
 F:50-540/Domain: cholinesterase homology
 F:221,455/Active site: Ser, His #status predicted

Query Match 37.8%; Score 1163; DB 2; Length 554;
 Best Local Similarity 44.3%; Pred. No. 1,9-83;
 Matches 241; Conservative 84; Mismatches 133; Indels 26; Gaps 7;

QY 16 LILLOPLGHRMGKTGPSAEGPQNRTRLGWIOGKQVTVLGSPPVNVNVLGVPAPAPLGS 75
 DB 16 LILLOPLGHRMGKTGPSAEGPQNRTRLGWIOGKQVTVLGSPPVNVNVLGVPAPAPLGS 75

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Db      11 LAVCFLIGH-----SLLEPVVDITGQKVLGKYSLEGEQPAVLEIGVFPAPKPLGS 62
QY      76 LRFNTPOPASPMNDLREATSYPNLCLONSEW---LLLDQHLKVHYPKFVSDCLYNY 133
Db      63 LRFAPPOAPBPMSVVKATTSYPPMCSQDGMATILSDMFSTEKEILLPLKISBDCLYNY 133
QY      134 APAAADUGSLPVLVWFPFGAFKTSASIFDGSALAAVEDLVVVVQYRLGIFGFTTWD 193
Db      123 SPADLTSSQLPVMVWHGGGLVIGGRSPYNGALSAHENVVYIIQYRLGIMGLFSTGD 182
QY      194 QHAPGNWAFKQVAAALSMVKNIIEFGGDPSSVTIFGSAGAISSVSLISPMAGLFLK 253
Db      183 EHSPPGMWHLDDQALALRWQDNIANFGNPDVTIIFGSSSGAISVSIVLSPKGLD.FHR 242
QY      254 AIMSGLVAILPYLEAHDIKESDLOVVAHFCGNNASDEALLRCICRTKPSKELLTIS 310
Db      243 AISESGVIVNTVNGKKNIQAVNEIATLSQC--NDTSAAMVQCLRKOTSELEISGKL 300
QY      311 -QKTSFTRVVDGAFPPNBPDLISQKAFKAISIIIGNHCEGFLPM--KEAPE-IL 365
Db      301 VOYNISLSTMDGVVLPKAPBEILAEKSFNTVPYIVFNKQBERGWIIPMMLQVLLPEGM 360
QY      366 SGNKSLALHLIQLNLIHPQYHLVANEYFHDGSLTEIRDSLDDLDLGDVFPVVALIT 425
Db      361 NBETASLLRRFHSBELNISSEMIPIAVIEQYLRGVDPKAKSELIDMFQDIFFGIPAVL 420
QY      426 ARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFKLGDIWEGATE 485
Db      421 SRSRLRDAGVSTYVYEFRRPSVSDKRPQVYBESDDEILFFVFGAPLTK-----EGASE 474
QY      486 EEKLSLRKMKKYATTPARTGNPNDLSLWPAVNLTEQYLOLDLNMISGQRLKBERVDW 545
Db      475 EETLSQVWKAFKFWANFARNGNPGBGLPHMPEYDEQEGYLQIGATTQQAQSLKAEVAFW 534
QY      546 TSTI 549
Db      535 TELL 538

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RESULT 7

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S19307
C:Species: carboxylesterase (EC 3.1.1.1) precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S19307; S23607
R:Matsumura, M.; Inoue, H.; Ichinose, M.; Tanaka, S.; Miki, K.; Kurokawa, K.; Takahashi
FEBS Lett. 293, 37-41, 1992
A:Title: The nucleotide and deduced amino acid sequences of porcine liver proline-beta-T
A:Reference number: S19307; MUID:92070571; PMID:1959668
A:Accession: S19307
A:Molecule type: mRNA
A:Residues: 1-566 <MAT1>
A:Cross-references: UNIPROT:Q29550; EMBL:X63323; NID:G1930; PIDN:CAA44929.1; PID:G1931
A:Accession: S23607
A:Molecule type: protein
A:Residues: 19-40 <MAT2>
A>Note: 28-Lys and 33-Leu were also found
C:Superfamily: cholinesterase; cholinesterase homology
F:1-18/Domain: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer
F:19-566/Product: signal sequence #status predicted <SIG>
F:19-566/Product: carboxylesterase #status experimental <MAT>
F:51-552/Domain: cholinesterase homology <CHE>
F:80/Binding site: carbonyl site: carbonyl (Asn) (covalent) #status predicted
F:222,467/Active site: Ser, His #status predicted

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Query Match

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Beat local Similarity 37.8%; Score 1162.5; DB 2; Length 566;
Matches 250; Conservative 71; Mismatches 202; Indels 41; Gaps 8;
QY      12 WCFPILOPLGHRQMGKTPSAGPQNRTRLGMIOGKQVTVLGSVPVNVFVGVPFAP 71
Db      2 WLLPLVLSLSSATW--AGOPASPPVVDTAQGVILGKYSLEGLAQVAVFLGVPFAP 59

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QY      72 PLGSIRFTNPOPASPMNDLREATSYPNLCLON-----SEWLLDQHLKVHYPKFVGS 124
Db      60 PLGSIRFAPPOAPBPMSVVKATTSYPPMCSQDGMATILSDMFSTEKEILLPLKISBDCLYNY 133
QY      125 EDCLYNIYAAAHADTSKLPVLVWFPFGAFKTSASIFDGSALAAVEDLVVVVQYRLG 184
Db      115 EDCLYNIYTPADLTTRKGRLPVVMWHGGGLVIGGAPMDGIVVLAHENVVVALQYRLG 174
QY      185 IFGFTTWDQHPGNWAFKQVAAALSMVKNIIEFGGDPSSVTIFGSAGAISSVSLIS 244
Db      175 IWGFFSTGDSHSGNMGHLDQVAAALHWVENIANFGGPGSVTIIFGSAGGESVSLIS 234
QY      245 PMAGLFLHKAIMSGVAILPYLEAHDIKESDLOVVAHFCGNNASDEALLRCICRTKPSK 304
Db      235 PLKAVLEHRAISSESGVALTVLVRKDKMA--AKQIVLACCKTTSAVFVHCLRKQSED 292
QY      305 ELLTISQKTSFT-----RYVDGAFPPNBPDLISQKAFKAISIIIGNHCEGFLPM-- 349
Db      293 ELLDITLKKKPLTLDPHGQGRSHFPLFTVVDGVALPMPBEILAEKDFNTVPYIYINK 352
QY      350 HECGFLPKKAPKAPILSGS-NKSLALHLION---ILHIPOYLHLVANEYFHDGSLTEI 405
Db      353 QERGMILFTMGFPPLSEKLDQKATSLMKSPYIANIPELIPVATDKLGSTDDPVK 412
QY      406 RUSLLDLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHDEV 465
Db      413 KDLFLDMDGVFVGPVSVTVARQHRDGAFTTMYEQRPSFSSDKKPTVIGDHGEIF 472
QY      466 FVFGAPLKGDIWVEGATEEELSKRMKYATTPARTGNPNDLSLWPAVNLTEQYLOLD 525
Db      473 SVFGFPLKGD-----APEEVSLSKTVWKFWANFARNGNPGBGLPHMPEYDEQEGYL 526
QY      526 QLDLNMISGQRLKBERVDWFTSTI 549
Db      527 QIGVNTQAKRLKGEVAFWINDLL 550

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RESULT 8

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JX0054
C:Species: carboxylesterase (EC 3.1.1.1) EI precursor, minor form - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Aug-1998
C:Accession: JX0054
R:Takagi, Y.; Morohashi, K.; Kawabata, S.; Go, M.; Omura, T.
J. Biochem. 104, 801-806, 1988
A:Title: Molecular cloning and nucleotide sequence of cDNA of microsomal carboxylesterase
A:Reference number: JX0054; MUID:89174514; PMID:3235453
A:Accession: JX0054
A:Molecule type: mRNA
A:Residues: 1-549 <YAK>
A:Experimental source: liver
C:Superfamily: cholinesterase; cholinesterase homology
F:1-18/Domain: carboxylic ester hydrolase; glycoprotein; microsome
F:19-549/Product: signal sequence #status predicted <SIG>
F:50-538/Product: carboxylesterase EI #status predicted <MAT>
F:79,274,302,375,476/Binding site: carbonyl site: carbonyl (Asn) (covalent) #status predicted
F:221,453/Active site: Ser, His #status predicted

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Query Match

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Beat local Similarity 37.2%; Score 1144; DB 2; Length 549;
Matches 238; Conservative 92; Mismatches 183; Indels 34; Gaps 9;
QY      16 LIIQPLGHRQMGKTPSAGPQNRTRLGMIOGKQVTVLGSVPVNVFVGVPFAP 75
Db      11 LAVCFLIGH-----PSSP-PVVDITGKVLGKYSLEGTQVAVFLGVPFAPKPLGS 62
QY      76 LRFNTPOPASPMNDLREATSYPNLCLON-----SEWLLDQHLKVHYPKFVSDCLY 128
Db      63 LRFAPPEAPBPMSVVKATTSYPPMCSQDGMATILSDMFSTEKEILLPLKISBDCLY 117
QY      129 YNIYAPAAHADTSKLPVLVWFPFGAFKTSASIFDGSALAAVEDLVVVVQYRLGIFG 188

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QY 468 FGCAFLKGDIVMEGATEEBEKLRSKMKYATPARTGNGNDLSLTPAYNLTEOYLQ 527
 Db 476 FGAPFLK-----EGASEEIRLSKVMKFMANFARNGNPNNGELPHPEYNQEGYLQI 529
 QY 528 DLNMSIGRLKEPRVDPMFTS 547
 Db 530 GANTQAQRLKKEVAFAFTN 549

RESULT 10

carboxylesterase (EC 3.1.1.1) ES-4 precursor, liver - rat
 N/Alternate names: hydrolyase B
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S62788; S51203; A55304; S49257
 R/Robbi: M. van Schaalingen, E. Beaufay, H.
 Biochem. J. 313, 821-826, 1996
 A/Title: Cloning and sequencing of rat liver carboxylesterase ES-4 (microsomal palmitoyl)
 A/Reference number: S62788; PMID:96190723; PMID:8611161
 A/Accession: S62788
 A/Molecule type: mRNA
 A/Residues: 1-561 <ROB>
 A/Cross-references: UNIPROT:Q64573; EMBL:X81825; NID:G550417; PIDD:CAAS7419.1; PID:G5504
 R/Morgan, B.W., Yan, B., Greenway, D., Petersen, D.R., Parkinson, A.
 Arch. Biochem. Biophys. 315, 495-512, 1994
 A/Title: Purification and characterization of two rat liver microsomal carboxylesterases
 A/Reference number: S51202; PMID:95077450; PMID:7986098
 A/Accession: S51203
 A/Molecule type: protein
 A/Residues: 19-48 <MOR>
 A/Experimental source: liver
 R,Yan, B., Yang, D., Brady, M., Parkinson, A.
 J. Biol. Chem. 269, 29688-29696, 1994
 A/Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, and re
 A/Reference number: A55304; PMID:95050819; PMID:7961958
 A/Accession: A55304
 A/Molecule type: mRNA
 A/Residues: 16, 'P', '61-212, 'A', 214-252, 'T', 254-309, 'IT', 312-341, 'N', 343-424, 'FY
 A/Note: the sequence in GenBank entry RNU10697, release 107, (PID:G562008) has the codon
 R/Robbi, M., Beaulieu, H.
 Submitted to the EMBL Data Library, September 1994
 A/Reference number: S49257
 A/Accession: S49257
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-561 <RO2>
 A/Cross-references: EMBL:X81825; NID:G550417; PIDD:CAAS7419.1; PID:G550418
 C/Function:
 A/Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion
 C/Superfamily: cholinesterase; cholinesterase homology
 C/Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver
 F/1-18/Domain: signal sequence #status predicted <SIG>
 F/19-561/Product: carboxylesterase ES-4 #status experimental <MAT>
 F/50-551/Domain: cholinesterase homology <CHE>
 F/221,466/Active site: Ser, His #status predicted
 F/301/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 37.0%; Score 1139; DB 2; Length 561;
 Best Local Similarity 43.4%; Pred. No. 1.5e-81;
 Matches 243; Conservative 82; Mismatches 195; Indels 40; Gaps 10;
 QY 15 FILLOPLIGHROMGTGSAEGPONTRLGWIQKQVTVLGPVNVVFLGVPAPAPLIG 74
 Db 5 FILVLSATCVVYG--NPSSP-PVVDITKRGVLRGKTVSLBSGVTSVAVFLGVFPAPPLIG 61
 QY 75 SLRFTNPDPASPMNDLRAATSYPMCLQNSFW-----LLLDQHLKTVHYKFGVSEDCY 129
 Db 62 SLRFPAPPAEPMWSFKVNTTTPMCSQDAKAGQRMNDLLTNREKIH---LEFSDCLY 118

QY 130 LNTVAPAHADTGSGLPVLWFPFGAGFTGSAJFDSALAAVEDVLVVVVOYRLGIFGFE 189
 Db 119 LNTVPAEDFTKNSRLPVMVWVHGGGMTLGGASTYDGRVLSAYENVVVAIQRLGIMGFE 178
 QY 190 TTWDQAPGNMAFPDQVAAVSWYQKNIIEFGGPPSSVTTFGSAAGISVSSILSPMAKG 249
 Db 179 STGDHSRGNWGHLDQVAAVHWQDNIANFGDPSVTLFGESAGGFSVYVLSPLTKN 238
 QY 250 LFHKAIMESGVAVIIPYLEANDYKESDLOVVAHFCGNNAADSEALLRCLRTKPSKELLTL 309
 Db 239 LFRALISESGVFLPGLTLTKDVRA--AKQIDMAGCETTSATVHCLRKQTEBELLEI 296
 QY 310 SQTKR-----SFRVYDGAFFPNEPLDLSQCAAFALSTIGVNNHECGF 354
 Db 297 MKKNNILKLSQQRDNKESYHFLSTVDNVLPDKDKELAEKNFTVPIYIGINKOECGW 356
 QY 355 LRP--KKEAPELLSSGNKSLAHLIQ--NLIHPQYLAHVANEYFHDKSLTEIRDSL 409
 Db 357 LFTMMGFVPAVE-LDKKMAITLLEKPSLYGIPEDIIIVAIERKKGSDSIKINDGI 415
 QY 410 LIDLGVFVFPVALITARYHRDAGAPVYFVEERRPQCFEDTKAFYKADHAEVRFVG 469
 Db 416 LAFIGVFSIPSVMVSRDHDAQAPTYMZYQYFSPSSPQRKXHVGDHADDLYSVFG 475
 QY 470 GAFKGDIVMEGATEEBEKLRSKMKYATPARTGNGNDLSLTPAYNLTEOYLQ 529
 Db 476 AFILK-----DGASEEIRLSKVMKFMANFARNGNPNRGLPHPQDQKEEYLQIGA 529
 QY 530 NMSIGRLKEPRVDPMFTSI 549
 Db 530 TTQOSORLKAEEVAFAFTQL 549

RESULT 11

carboxylesterase (EC 3.1.1.1) egaeyn - mouse
 N/Alternate names: beta-glucuronidase endoplasmic reticulum-targeting protein; esterase-
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
 C/Accession: A55281
 R/Ovnic, M.; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; Heintz, N.; C
 Genomics 11, 956-967, 1991
 A/Title: Characterization and functional expression of a cDNA encoding egaeyn (esterase-
 A/Reference number: A55281; PMID:92147141; PMID:1783403
 A/Accession: A55281
 A/Status: preliminary
 A/Molecule type: mRNA; protein
 A/Residues: 1-562 <OVN>
 A/Cross-references: UNIPROT:Q64176; GB:S80191; NID:G244727; PIDD:AAH2133.1; PID:G244728
 A/Note: sequence extracted from NCBI Backbone (NCBI:80191, NCBI:P:80194)
 C/Superfamily: cholinesterase; cholinesterase homology
 C/Keywords: carboxylic ester hydrolase; endoplasmic reticulum
 F/51-552/Domain: cholinesterase homology <CHE>
 F/222,467/Active site: Ser, His #status predicted

Query Match 37.0%; Score 1138.5; DB 2; Length 562;
 Best Local Similarity 44.4%; Pred. No. 1.6e-81;
 Matches 240; Conservative 76; Mismatches 195; Indels 29; Gaps 6;
 QY 31 GSAEGPONTRLMIOGQVTVLGPVNVVFLGVPAPAPLIGSLRFTNPDPASPMNDL 90
 Db 19 GHSPSPMVDVTDGKVLGKTVSLSGFTQVAVFLGVPAPAPLIGSLRFPAPPAEPMWSV 78
 QY 91 REATSYPMCLQNSFWLLDQHLKTVHYKFGV--SEDCLYNTVAPAHADTGSGLPVLV 148
 Db 79 KNATSYPMCGDQPVGQIYNDLLTNREKIPLOFSEDCLYNTTPDLYTSDMLPVMV 138
 QY 149 WFPGAFKTSASIFDGSALAAVEDVLVVVVOYRLGIFGFTTWOQHAPGNMAFPDQVAA 208
 Db 139 WIRGGGLVAGASTYGVVSTHENVVVIQYRLGIMGFSYGDHSRGNWGHLDQVAA 198
 QY 209 LSWQKNIIEFGGPPSSVTTFGSAAGISVSSILSPMAKGLFHKAIMESGVAVIIPYLEA 268

Db 199 LHMVQDNIAGKGGPGSVTTIGESAGGESVVLVLSPLAKRLFORAISEGVALTAGLVK 258
 Qy 269 HDYKSESDLOVVAHFCGNMADSSEALRLCLRTKPSKELLTLOSRTKSE----- 316
 Db 259 KNTREPLAEKIAVIGGCKN--TTSAAWHCHLQKTEBELLGTTLKLNLFKDLHGDSDRSH 316
 Qy 317 ---TRVVDGAFPPNEPDLDSOKAFKAIPISTIIGVNNHECGFLP-MKEAPEILSGNSKL 372
 Db 317 PFVPTLVLDGVLPRKMEBELLAERKNFNTVPIVGINKEFGWILPLTMNMYPPSDVVLQDMT 376
 Qy 373 ALHLIQN---LHHPQVYLVANEFYHDKSLTEIRDSLLDLDGVFFVVPALITARYH 429
 Db 377 AMSLLKSSFFLNLPEDAIIVAEIKYLRDKQYTGKRNQDLLELIGDVVFGVPSVIVSKGH 436
 Qy 430 RDAGAPVYFVEFRFRPOCFEDTKPAFVAKADAEVRFEVFGAFKGDIVMEGATEEERKL 489
 Db 437 RDAGAPVYFVEFRFRPOCFEDTKPAFVAKADAEVRFEVFGAFKGDIVMEGATEEERKL 490
 Qy 490 LSRDMKYMATFARTGPNNGNDLSLMPAYNLTEQYLQDLNMSLGQRLEKPRVDFTSTI 549
 Db 491 LSKMMKFMANFARNGNPNCGGLPHMPEYDQEGYLGATTTQQAOKLKEKVAFWTELL 550

RESULT 12

A:1584
 A:1584 carboxylesterase (EC 3.1.1.1) precursor - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 21-May-1990 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
 C:Accession: A31584
 R:Long, R.M.; Satoh, H.; Martin, B.M.; Kimura, S.; Gonzalez, F.J.; Pohl, L.R.
 Biochem. Biophys. Res. Commun. 156, 866-873, 1988
 A:Title: Rat liver carboxylesterase: cDNA cloning, sequencing, and evidence for a multi-
 A:Reference number: A31584; MUID:89050119; PMID:2973315
 A:Accession: A31584
 A:Molecule type: mRNA
 A:Residues: 1-540 <LON>
 A:Cross-references: UNIPROT:P10959; GB:M20629; GB:X13587; NID:G203279; PIDN:AAA0871.1;
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein
 F:1-9/Domain: signal sequence #status predicted <SIG>
 F:10-540/Product: carboxylesterase #status predicted <MAT>
 F:41-529/Domain: cholinesterase homology <CH>
 F:70,265,266,293,366,467/Binding site: carbonyl hydrate (Asn) (covalent) #status predicted
 F:212,444/Active site: Ser, His #status predicted

Query Match 36.9%; Score 1136; DB 2; Length 540;
 Best Local Similarity 43.3%; Pred. No. 2.4e-81;
 Matches 237; Conservative 91; Mismatches 185; Indels 34; Gaps 9;
 Qy 16 LILQPLGHRQWKGTPSAGPQNRTRLGWIOGKOVTVLGSPPVNVFLGVFPAAAPPLGS 75
 Db 2 LAVCPIMCH-----PSSP-PVVDITTKGKVLGKTVSLGEGTQVYAVFLGVPFAKPPRGS 53
 Qy 76 LRFNTPOPASPMNLREATSYNLCLON-----SEWLLLDQMLKVHPKFGVSDCL 128
 Db 54 LRFAPPEPAEPMSFVKQTTTTPPMCSQDGVGKLLADWLSTGESIPLEF-----SEDC 108
 Qy 129 YLNTIYAPHADTGSKLPLVLPFGGAFKTSASIFDGSALAAEDVYLVVYQYRLGITGF 188
 Db 109 YLNTYSPADLTGKSRLLPVMVVIHGGGLIIGASPSGLTASAHENVVVVTIYQYRIGFGL 168
 Qy 189 FTTTDOHAPGMAFADQVVAALSWYQKNIFFGSDPSVTIIFGESAGAISVSLISPMAX 248
 Db 169 PSTGDHSRGMWALDQALALRWQDNIANFGCNPDSITIFGESAGISVSALVLSPLAK 228
 Qy 249 GLFKAIMESGVAIIPYLEAHDEKSEDLQVVAHFCGNMADSSEALRLCLRTKPSKELLT 308
 Db 229 NLFRAISESGVVLTTNLDKKNQAV--AQMIATLSGCGNNTSSAAMVCLCKQTEABELL 286
 Qy 309 LSKR--TTSFRVVDGAFPPNEPDLDSOKAFKAIPISTIIGVNNHECGFLP-MKEAPEILS 366
 Db 287 LTVLDMTSMSTVIDGVLPKTPPEILTEKSFNTVPIVGINKEFGWILPLTMNMGNTLSL 346

Qy 367 G-SNKSIALHLIQN---LHHPQVYLVANEFYHDKSLTEIRDSLLDLDGVFFVVP 422
 Db 347 GRNMKMASSFLKRFSPNMLISEVPAIIEKRLGTDDPAKKELLDMFSDVFFGIPV 406
 Qy 423 LITARYRDGAPVYFVEFRFRPOCFEDTKPAFVAKADAEVRFEVFGAFKGDIVMEG 482
 Db 407 VLMSRLDAGAPVYFVEFRFRPOCFEDTKPAFVAKADAEVRFEVFGAFKGDIVMEG 460
 Qy 483 ATTEERKLSSRMMKYMATFARTGPNNGNDLSLMPAYNLTEQYLQDLNMSLGQRLEKPRV 542
 Db 461 ASEETNLSLKVNMKFMANFARNGNPNCGGLPHMPEYDQEGYLGATTTQQAOKLKEKBEV 520
 Qy 543 DFWTSTI 549
 Db 521 AFWTELL 527

RESULT 13

A:1597
 A:1597 carboxylesterase (EC 3.1.1.1) precursor, liver - rat
 N:Alternate names: hydrolase C
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
 C:Accession: S71597
 R:Yan, B.; Yang, D.; Parkinson, A.
 Arch. Biochem. Biophys. 317, 222-234, 1995
 A:Title: Cloning and expression of hydrolyase C, a member of the rat carboxylesterase faml
 A:Reference number: S71597; MUID:95177656; PMID:7872768
 A:Accession: S71597
 A:Status: not compared with conceptual translation
 A:Residues: 1-561 <YAN>
 A:Molecule type: mRNA
 A:Experimental source: liver; endoplasmic reticulum
 C:Function:
 A:Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-561/Product: carboxylesterase #status predicted <MAT>
 F:50-551/Domain: cholinesterase homology <CH>
 F:558-561/Region: endoplasmic reticulum retention signal
 F:79,301/Binding site: carbonyl hydrate (Asn) (covalent) #status predicted
 F:221,466/Active site: Ser, His #status predicted

Query Match 36.7%; Score 1129.5; DB 2; Length 561;
 Best Local Similarity 43.4%; Pred. No. 8.3e-81;
 Matches 236; Conservative 83; Mismatches 188; Indels 37; Gaps 9;
 Qy 31 GPSAEGPQNRTRLGWIOGKOVTVLGSPPVNVFLGVFPAAAPPLGS LFTNPQASPMNLT 90
 Db 18 GNPSPPVVDITTKGKVLGKTVSLGEGTQVYAVFLGVPFAKPPRGS LRFAPQAPMPSFV 77
 Qy 91 REATSYNLCLONSEW-----LILDDQMLKVHPKFGVSDCLYLNTPAHADTGSKL 145
 Db 78 KNTTTPPMCSQDQTKQRNMDLTITNKEKVN--LQFSEDCYLNITTPADFTKDSRMP 134
 Qy 146 VLWVFGGAFKTSASIFDGSALAAEDVYLVVYQYRLGITGFPTTDOHAPGMAFADQ 205
 Db 135 VMVVIHGGGLTGGASITDGVLSAYENNVVAIQYLGITGFFSTGDHSRGMWALDQ 194
 Qy 206 VVALSWYQKNIFFGSDPSVTIIFGESAGAISVSLISPMAXGLFKAIMESGVAIIPY 265
 Db 195 VVALHWMQDNIANFGCNPDSITIFGESAGISVSALVLSPLAKNLYHRAISESGVVLITQ 254
 Qy 266 LEAHDEKSEDLQVVAHFCGNMADSSEALRLCLRTKPSKELLTSSQK-----TK 314
 Db 255 LFTYDVRPA--AKQIAPMACCKTTTSAIVHCLQKTEBELLEIMKRNLIKUSSQDRTK 312
 Qy 315 S-----FTRVVDGAFPPNEPDLDSOKAFKAIPISTIIGVNNHECGFLP-MKEAPEILSGS 368
 Db 313 ESHYFLSTVIDDVLPDQPKELIAERKNFNTVPIVGINKECGWLLTPMKRFPVDPVK-L 371
 Qy 369 NKSIALHLIQ---LHHPQVYLVANEFYHDKSLTEIRDSLLDLDGVFFVVPALIT 425


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Db      372 DKXKATMLEKESIVYCPEDIPVAIBKRGSDDPITIRGICILAFJGDLFCIPSVTV
Qy      426 ARYRDAGAVYEFYEFRRPQCEDDKPAFVADNADAEVRFYFGAFKGIWMEGATE
Db      432 SRDRDAGAPTYEYEQYVPSFSSPQRKDVGDHADDVYVFAGPIRL-----DGASE
Qy      486 EELKLRKMKKATATFARFNGNDLSMPAYNLTEQYLODLMNLSGRLKEPRDPM
Db      486 EELKLRKMKKATATFARFNGNDLSMPAYNLTEQYLODLMNLSGRLKEPRDPM
Qy      546 TSTI 549
Db      546 TOLL 549

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RESULT 14

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JC2447
C:Species: Rattus norvegicus (Norway rat)
C>Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C/Accession: JC2447; S23462
R:Robbi, M.; Beaufay, H.
Biochem. Biophys. Res. Commun. 203, 1404-1411, 1994
A>Title: Cloning and sequencing of rat liver carboxylesterase ES-3 (EGASYN).
A/Reference number: JC2447; MUID:95032008; PMID:7945287
A/Accession: JC2447
A/Molecule type: mRNA
A/Residues: 1-561 <ROB>
A/Cross-references: UNIPROT:Q63108; GB:X81395; NID:9550146; PIDN:CAA57518.1; PID:9550147
A/Experimental source: liver
R:Medda, S.; Proia, R.L.
Eur. J. Biochem. 206, 801-806, 1992
A>Title: The carboxylesterase family exhibits C-terminal sequence diversity reflecting
A/Reference number: S23460; MUID:92299008; PMID:1606962
A/Accession: S23462
A/Status: Preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 503-554, 'R', 556-561 <MED>
A/Cross-references: EMBL:X65295; NID:957557; PIDN:CAA46390.1; PID:957558
C/Keywords: carboxylic ester hydrolase; cholinesterase homology
F/1-18/Domain: signal sequence #status predicted <SIG>
F/19-561/Product: carboxylesterase ES-3 #status predicted <MAT>
F/50-551/Domain: cholinesterase homology <CHE>
F/79,107,489/Binding site: carboxylate (Asn) (covalent) #status predicted
F/221,466/Active site: Ser, His #status predicted

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Query Match

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Best Local Similarity 36.5%; Score 1123; DB 2; Length 561;
Matches 245; Conservative 86; Mismatches 193; Indels 56; Gaps 11;

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Qy      13 CFFLIQPLGHRQWKTGSAEGPQRNRLTGIOKQTVYGVVNVNVLGVFAAP 72
Db      2 CLVYLIVFLAFAAG--GHRSSLPVVDLTQGVKGLKYSLSGFTQPAVFLGVFAAP 59
Qy      73 LGSIRFPNPPASPMNLRBATSYPNLCUN-----SEVLLDQMLKXHPK 121
Db      60 LGSIRFPNPPASPMNLRBATSYPNLCUN-----SEVLLDQMLKXHPK 121
Qy      122 GVSDELTYNTIYAPAHADTGSKLPLYVMPFGAFKTSASIFDSGALAAVEDLVVVQY 181
Db      113 --SEDCLYNTIYTPDLTRKDLPLVWVHGGGLVFGASVYDGLASTHENVVVVVQY 170
Qy      182 RLGIREFFTQOHAPGNWAFDOVALSWYQNIIEFFGDPSSVTIFGSSAGLSVSL 241
Db      171 RLGIREFFTQOHAPGNWAFDOVALSWYQNIIEFFGDPSSVTIFGSSAGLSVSL 241
Qy      242 IISPAKGLFKAIVSGVALIIPY--EAHDVKESEDQVVAHCGNNAADSEALLRCLRT 300
Db      231 VLSPLAKMLFKAISSGVNLTAGLVKNTRPILAELKAAVVS---GCKSTTSASMVHCLQ 287
Qy      301 KPSKELTSLGKTSFT-----RVVDGAFPPNBPDLGLSGKAFKAIPIII 345

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Db      288 KTEBELTTLTKNLIFSIDLHGSRSQYPPVYVLOGVLPKPEBELLAKQNTVYIV 347
Qy      346 GVNNECCGFLP--MKEAPBELLSGNSKSLAHLQN---ILHIPPQYHLVANEYFHDKS 401
Db      348 GINKQEFQWILPTMANPBPDSMDKLDPMATATSLTKSSPLNLPBEALIPVAVEKYLRTDD 407
Qy      402 LTELRLSLDLGLVFVVPALITARYHRDAGAPVYEFRRPQCEDDKPAFVKADHA 461
Db      408 PDRNKDQLELIDVIFGVPSIVSRGHRDAGARTYMEFQYRPSFSKMKPSTVGDG 467
Qy      462 DEVAFVFGAFKGLDYMFEAGATEBEKLSRKMKATATPARTGNPNNDLSMPAYLT 521
Db      468 DEIVSVGAPRLG-----GTSKEINLSRKMKFMNANFANGPNQGLPHMPEYDQK 521
Qy      522 EGYLODGLATTQQAQKLKEKVAFMSE-----LWAKKPLHA 556
Db      522 EGYLODGLATTQQAQKLKEKVAFMSE-----LWAKKPLHA 556

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RESULT 15

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S10367
C:Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C/Accession: S10367; S12468; S51202; S23460; S14361
R:Robbi, M.; Beaufay, H.; Octave, J.N.
Biochem. J. 269, 451-458, 1990
A>Title: Nucleotide sequence of cDNA coding for rat liver pi 6.1 esterase (ES-10), a car-
A/Reference number: S10367; MUID:90351366; PMID:2386485
A/Accession: S10367
A/Molecule type: mRNA
A/Residues: 1-565 <ROB1>
A/Cross-references: UNIPROT:Q9R135; EMBL:X51974
A/Note: 168-Gln, 247-Lys, 423-Met, and 506-Asn were also found
A/Note: the sequence from Fig. 4 is inconsistent with that from Fig. 5 in having 265-Lys,
submitted to the EMBL Data Library, February 1990
A/Reference number: S12468
A/Accession: S12468
A/Molecule type: mRNA
A/Residues: 1-264, 'R', 266-565 <ROB2>
A/Cross-references: EMBL:X51974; NID:956898; PIDN:CAA3236.1; PID:956899
R:Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A.
Arch. Biochem. Biophys. 315, 495-512, 1994
A>Title: Purification and characterization of two rat liver microsomal carboxylesterases
A/Reference number: S51202; MUID:95077430; PMID:7986098
A/Accession: S51202
A/Molecule type: protein
A/Residues: 19-48 <MOR>
R:Medda, S.; Proia, R.L.
Eur. J. Biochem. 206, 801-806, 1992
A>Title: The carboxylesterase family exhibits C-terminal sequence diversity reflecting ct
A/Reference number: S23460; MUID:92299008; PMID:1606962
A/Accession: S23460
A/Status: Preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-185, 'Q', 187-422, 'M', 424-505, 'N', 507-565 <MED>
A/Cross-references: EMBL:X65296; NID:957553; PIDN:CAA46391.1; PID:957554
R:Gaustad, R.; Sletten, K.; Lovhaug, D.; Fonnun, P.
Biochem. J. 274, 693-697, 1991
A>Title: Purification and characterization of carboxylesterases from rat lung.
A/Reference number: S14361; MUID:91190080; PMID:2012599
A/Accession: S14361
A/Molecule type: protein
A/Residues: 19-26, 'P', 28-37 <GAU>
C/Suprafamily: cholinesterase; cholinesterase homology
C/Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer
F/1-18/Domain: signal sequence #status predicted <SIG>
F/19-565/Product: carboxylesterase #status predicted <MAT>
F/50-551/Domain: cholinesterase homology <CHE>
F/79,489/Binding site: carboxylate (Asn) (covalent) #status predicted

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F:221,466/Active site: Ser, His #status predicted

Query Match 36.4%; Score 1121.5; DB 2; Length 565;

Best Local Similarity 42.4%; Pred. No. 3.6e-80;

Matches 245; Conservative 79; Mismatches 199; Indels 55; Gaps 11;

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OY      12 WCFLLIQLPGLGHROWGKTGPSAEGPQNRTRIGMIQSKQVTVLGSPPVNNVFLGVFPAAP 71
      8 WLF-----LAACFAMGY--PSSP--PVNTVTKGVTKGVNLEGFAPQPAVAVLGIPIFAKP 58
DB      72 PLGSIRFTNPQASPMWDLUREATSYPNLCQN-----SEWLLDDQMLKHYHPKFGVS 124
      59 PLGSIRFAPQPAEPMNVFKNTSTYPMCSODAVGGQVLSLFTNKENIPIQF-----S 113
OY      125 EDCLYNTIYAPAHADTGSKLPLYVWFPGCAFKTGSASIFDGSALAAEDVLVWVQYRLG 184
      114 EDCLYNTIYTPADLTKNRLPFWVWIRHGGGLVVGASITDGOVLSAHENVVVTIQRRLG 173
DB      185 IFFFTTWDOHAPGNWAFKQVVALSWQNIIEFFGDPSSVTIFGESAGAISVSLLIS 244
      174 IWFSTGTDEHSGWGHLDQVAAALHWQDNINANGNGSVTIFGESAGGFSVSALVLS 233
OY      245 PMAKGLFHKAIMESGVALIIPYIEADYKESDLOVVAHFCGNNAADSEALLRCLRTPESK 304
DB      234 PLAKKLFHRAISESGVLTSLALITTDKRIANL--IATLSGCKTTSAVMVHCLKQKTED 291
OY      305 ELLTSSOKTKSF-----TRVVDGAFPPNBPDLDSOKAFKAIPSIIGVNN 349
DB      292 ELLETSLKLANPKLDLGNPKESYPLPTVIDGVLPKTPETILAKSFNTVPIYIGINK 351
OY      350 HECGFLPMKSAPELLSG-----SNKSLALHLIQNLHIIPQYLHLVANEYFHDKSLTE 404
DB      352 QEFGWIIPTLMGYPISEGLDQKTAKSLLWKSYPYTKISEKMIPIVAEKYCGTDDPAK 410
OY      405 IRDSLDDLGVYFVVPALITARYHDAAGAPVYIEFRRHPQCEBDTKPAFYKADHADEV 464
DB      411 RKDLFPQDLVADVIFGVPSVWVSRSHRDGAPTFMYEFERPSFVSAMRPKTVIGDHGDEL 470
OY      465 RFVFGCAFLKGDIVMPEGATEEEKLSRMMKCYWATPARTGNPGNDLSLMPAYNLTEOY 524
DB      471 RSVFGSPFLK-----DQASEETNLSKVMKYMANKYANFANGSPNGGGLPHMPEYDQKEGY 524
OY      525 LQDLNMSIGORLKEPRVDFTWTSTIPLILSADMHLSP 562
DB      525 LKIGASTQAQORLKDKEVAFWSE-----LRAKEAAEBP 557
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Search completed: June 16, 2005, 20:45:45

Job time : 45 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2005, 20:27:00 ; Search time 179 seconds
(without alignments)
1662.112 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 3079
Sequence: 1 MPQGLTSSASQWCFILQP.....PLSLRFLSLQPFPCAP 581

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2915	94.7	575	2	Q6NTJ32
2	2606	84.6	525	2	Q6DNG9
3	2454	79.7	469	2	Q6N8C9
4	2250	73.1	575	2	Q6AW47
5	2094.5	68.0	575	2	Q6AW46
6	1985	64.5	545	2	Q6I034
7	1676.5	54.4	361	2	Q95KH3
8	1298.5	42.2	557	1	SASB_ANAPL
9	1283.5	41.7	561	2	Q91W60
10	1281	41.6	559	2	Q6BK48
11	1276.5	41.5	559	2	Q35533
12	1271	41.3	559	2	Q6BM97
13	1266.5	41.1	556	2	Q6PDB7
14	1263.5	41.0	568	2	Q6GMS4
15	1262.5	41.0	561	2	Q70177
16	1260.5	40.9	560	2	Q6R097
17	1257.5	40.8	554	2	Q35535
18	1239.5	40.3	562	2	Q6P306
19	1238	40.2	558	2	Q6K3R0
20	1233.5	40.0	558	2	Q6QZ83
21	1233.5	40.0	532	1	EST2_RABIT
22	1230	39.9	559	1	EST2_HUMAN
23	1213.5	39.4	561	2	Q70631
24	1213.5	39.4	566	2	Q766D7
25	1213.5	39.4	566	2	Q6E4S9
26	1210.5	39.3	557	2	Q6A0T6
27	1199	38.9	561	1	EST1_MESAU
28	1191	38.7	586	2	Q61PK9
29	1187.5	38.6	568	2	Q6PG74
30	1187.5	38.6	572	2	Q810S9
31	1186.5	38.5	554	1	ESTM_MOUSE

32	1183	38.4	565	2	Q95N05
33	1179.5	38.3	571	2	Q6UW08
34	1179	38.3	568	2	Q726J1
35	1175	38.2	565	2	Q8TD29
36	1171.5	38.0	568	2	Q8VCU1
37	1169.5	38.0	561	2	Q91W60
38	1164	37.8	565	2	Q97582
39	1162.5	37.8	555	2	Q6GMJ1
40	1162.5	37.8	566	1	EST1_PIG
41	1159.5	37.7	566	2	Q464Z1
42	1150.5	37.4	565	1	EST1_RABIT
43	1150	37.3	564	2	ESTN_MOUSE
44	1149	37.3	565	2	Q35534
45	1144	37.2	549	1	EST1_RAT

ALIGNMENTS

RESULT 1	ID	Q6NTJ32	PRELIMINARY;	PRT;	575 AA.
AC	Q6NTJ32	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)				
DE	FLJ31547 protein.				
GN	Name=FLJ31547;				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PCR rescued clones;				
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Ditchenko L., Marusik K., Farmer A.A., Rabin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,				
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Rhodes S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahy J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krywinski M.I., Skolnik U., Small D.E., Scherch A., Schein J.E.,				
RA	Jones S.J., Maitra M.A.,				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PCR rescued clones;				
RC	Director MGC Project;				
RL	Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.				
CC	-i- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.				
DR	EMBL; BC069501; AA069501.1; -				
DR	HSPB; P12337; I4Y.				
DR	GO; GO:0003824; F:catalytic activity; IEA.				
DR	InterPro; IPR002018; Carboxylesterase.				
DR	InterPro; IPR00379; Ser esters.				
DR	Pfam; PF00135; Coesterase; 1.				
DR	PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.				
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.				
KW	Hydrolase.				
SC	SEQUENCE 575 AA; 63926 MW; 6F5B735BDEFC9C09 CRC64;				

QY 151 PGAFKTSASIFDGSALAAVEDVLVVVVOYRLGIFGFTTMDQHPAGNMAFKQVAAIS 210
 DB 145 PGAFKTSASIFDGSALAAVEDVLVVVVOYRLGIFGFTTMDQHPAGNMAFKQVAAIS 204
 QY 211 WVGKRIEFGDPSVITFGESAGASISVLSLSMAGLTHKAIMESGVAIIIPYLEAND 270
 DB 205 WVGKRIEFGDPSVITFGESAGASISVLSLSMAGLTHKAIMESGVAIIIPYLEAND 264
 QY 271 YKESBDLVVAHFCNNASDSEALRCRTKPSKELLTQSOKTSFTRVVQGAFFPNEPL 330
 DB 265 YKESBDLVVAHFCNNASDSEALRCRTKPSKELLTQSOKTSFTRVVQGAFFPNEPL 324
 QY 331 DLSQKAFKAIPIIIVNNHECGFLPMKEAPEILSGNSKSLALHILIONLHIPEOYLAL 390
 DB 325 DLSQKAFKAIPIIIVNNHECGFLPMKEAPEILSGNSKSLALHILIONLHIPEOYLAL 384
 QY 391 VANEFYHDKSLTEIRDSLLDLGDFVFPVLPALITARYHRDAGAVYVEFRHPRQCED 450
 DB 385 VANEFYHDKSLTEIRDSLLDLGDFVFPVLPALITARYHRDAGAVYVEFRHPRQCED 424
 QY 451 TKPAPVADHADVAFVFGAFLKGDIVMPEGATEEKLRSKMKYATFARTGNPKN 510
 DB 425 -----BQATEEKLRSKMKYATFARTGNPKN 454
 QY 511 DLSLMPAYNLTEOYLQDLNMSLQRLKEPRVDFTSTIPILSASDMLHSPSSLTFLS 570
 DB 455 DLSLMPAYNLTEOYLQDLNMSLQRLKEPRVDFTSTIPILSASDMLHSPSSLTFLS 514
 QY 571 LLQPEFFFCAP 581
 DB 515 LLQPEFFFCAP 525

RESULT 3

Q8NBC8 PRELIMINARY: PRT; 469 AA.
 AC Q8NBC8;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein FLJ33678.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_Taxid=9606;
 RX TISSUE=Brain;
 RC Pubmed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 Sekine M., Ohsawa H., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y., Ishida S.,
 Ono Y., Takiguchi S., Watanabe S., Yosiida M., Hotuta T., Kusano J.,
 Kanohori K., Takahashi-Fuji A., Hara H., Tanase T., Nomura Y.,
 Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 Musashino K., Yuki H., Oshima A., Sasaki N., Hotsuka S.,
 Yoshikawa K., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 Moriya S., Momiyama H., Satoh N., Takami S., Teraishi Y., Suzuki O.,
 Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y., Okamoto S.,
 Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema T., Okamoto S.,
 Ohtsuka R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 CC -1 SMILARITY: Belongs to the type-B carboxylesterase/1lipase family.
 DR EMBL; AK090997; BAC03565.1; -.
 DR HSPB; P12337; 1K4Y.
 DR CO; G0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000379; Ser_estr.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KM Hydrolyase.
 SQ SEQUENCE 469 AA; 52312 MW; 7A186F68C10A9080 CRC64;

Query Match 79.7%; Score 2454; DB 2; Length 469;
 Best Local Similarity 99.6%; Pred. No. 7.8e-179;
 Matches 467; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 113 MLKHYPRFGVSECLYINIAPAHADTGSRLPLVWFPFGAFKTSASIFDGSALAAVE 172
 DB 1 MLKHYPRFGVSECLYINIAPAHADTGSRLPLVWFPFGAFKTSASIFDGSALAAVE 60
 QY 173 DVLVVVOYRLGIFGFTTMDQHPAGNMAFKQVAAISWVGKRIEFGDPSVITFGES 232
 DB 61 DVLVVVOYRLGIFGFTTMDQHPAGNMAFKQVAAISWVGKRIEFGDPSVITFGES 120
 QY 233 AGAISVSLISPMNAKGLFHKAIMESGVAIIPLYEADHYKESBDLVVAHFCNNASDSE 292
 DB 121 AGAISVSLISPMNAKGLFHKAIMESGVAIIPLYEADHYKESBDLVVAHFCNNASDSE 180
 QY 293 ALPCLRTKPSKELLTQSOKTSFTRVVQGAFFPNEPLDLSQKAFKAIPIIIVNNHEC 352
 DB 181 ALPCLRTKPSKELLTQSOKTSFTRVVQGAFFPNEPLDLSQKAFKAIPIIIVNNHEC 240
 QY 353 GFLPMKEAPEILSGNSKSLALHILIONLHIPEOYLHVAHNEFYHDKSLTEIRDSLLD 412
 DB 241 GFLPMKEAPEILSGNSKSLALHILIONLHIPEOYLHVAHNEFYHDKSLTEIRDSLLD 300
 QY 413 LGDVFVFPVLPALITARYHRDAGAPVYFEFRHPRQCFEDTKAPYKADHADVRFVFGAF 472
 DB 301 LGDVFVFPVLPALITARYHRDAGAPVYFEFRHPRQCFEDTKAPYKADHADVRFVFGAF 360
 QY 473 LKGDIVMEGATEEKLRSKMKYATFARTGNPNDLSLMPAYNLTEOYLQDLNMS 532
 DB 361 LKGDIVMEGATEEKLRSKMKYATFARTGNPNDLSLMPAYNLTEOYLQDLNMS 420
 QY 533 LGQRLKEPRVDFTSTIPILSASDMLHSPSSLTFLSLLQPEFFFCAP 581
 DB 421 LGQRLKEPRVDFTSTIPILSASDMLHSPSSLTFLSLLQPEFFFCAP 469

RESULT 4

Q6AW47 PRELIMINARY: PRT; 575 AA.
 AC Q6AW47;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Carboxylesterase-like urinary excreted protein.
 GN Name=cuxin;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_Taxid=9615;
 RX TISSUE=urine;
 RC Pubmed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 Sekine M., Ohsawa H., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y., Ishida S.,
 Ono Y., Takiguchi S., Watanabe S., Yosiida M., Hotuta T., Kusano J.,
 Kanohori K., Takahashi-Fuji A., Hara H., Tanase T., Nomura Y.,
 Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 Musashino K., Yuki H., Oshima A., Sasaki N., Hotsuka S.,
 Yoshikawa K., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 Moriya S., Momiyama H., Satoh N., Takami S., Teraishi Y., Suzuki O.,
 Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y., Okamoto S.,
 Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema T., Okamoto S.,
 Ohtsuka R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL: AB186392; BAD35015.1; -.
 DR GO: GO:0003824; F:catalytic activity; IEA.
 DR InterPro: IPR002018; Carboxylesterase.
 DR pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 575 AA; 63620 MW; 1005C3582E1183D CRC64;

Query Match 73.1%; Score 2250; DB 2; Length 575;
 Best Local Similarity 75.7%; Pred. No. 4e-163;
 Matches 417; Conservative 61; Mismatches 73; Indels 0; Gaps 0;

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QY 31 GPSAEGQQRNTRLGKQVTVLGSPPVNVFLGVFPAPPLGSRFTNPPQASWMDL 90
DB 25 GPADADAVRSTRIGLVGKQATVLSGTMVNVFLGIPFAAPPLGPIRFKRPKPFALLMDS 84
QY 91 REATSYPNLCLQNSEMLLDQHLKHYPKFGVSEDCLYNLYAPAHADTSGKLPVLMF 150
DB 85 RDAITSYKCLQNSWMLSDQHLKHYPNLVESEDCLYNLYAPAHANTSGKLPVLMF 144
QY 151 PGGAFTGASIFDGSALAAVEDVLVYVYRLGIFGFTTWDQAPGMAFKQVALS 210
DB 145 PGGAFTGASIFDGSALAAVEDVLVYVYRLGIFGFTTWDQAPGMAFKQVALS 204
QY 211 WYQKNIFFGQDPSVTITGSGAGASVSSLLSPMAKGLPKAKIMESGVAIIPYLEAH 270
DB 205 WYQKNIFFGQDPSVTITGSGAGASVSSLLSPMAKGLPKAKIMESGVAIIPYLEAH 264
QY 271 YKESGELQVVAHFCGNNAASDEALRLCTKPKSKELTLISOKTSFRRVNDGAFRRPE 330
DB 265 DENEDLQVIARIICGVNSDVALLOCLRAKSSSELDLANKTISFRVNDGAFRRPE 324
QY 331 DLISQKAFAPSIIGVNNHEGFLPMKEAPEILSGNSKSLALHLIQLNLTIPPQYLHL 390
DB 325 DLITKTRPSISVIGVNNHEGFLPMKEAPEILSGNSKSLALHLIQLNLTIPPQYLHL 384
QY 391 VANEFYHDKSLTEIRDSLIDLGLGVFPVVPALITARYHNDAGAPVYFYFRRPQCFED 450
DB 385 VADQFYVKKHSPIVEIRDSFLDLGVFPVVPALITARYHNDAGAPVYFYFRRPQCFED 444
QY 451 TKPAVVKADHDEVRFVVGGAFLKGLDYMFGATEEKKLSRQMKWMAFARTGNPN 510
DB 445 TRPAFVADHSDERFVVGGAFLKGLDYMFGATEEKKLSRQMKWMAFARTGNPN 504
QY 511 DLSMPAYNLTQYQLDLNMSLGQRLKEPRVDPMFTSTIPLISASDMLHSPSSITFL 570
DB 505 GLPLMPAYSQSEYQLKLDLNIISVQKLKEQVEVFMSTDLPLIMSWSTADPGPVPLSIS 564
QY 571 LLOPFFFCAP 581
DB 565 VLDPFLSSAP 575

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RESULT 5

Q6AM46 PRELIMINARY; PRT; 575 AA.

AC Q6AM46; DT 25-OCT-2004 (T-EMBLrel. 28, Created) DT 25-OCT-2004 (T-EMBLrel. 28, last sequence update) DE Carboxylesterase-like urinary excreted protein. GN Name=cauxin; OS Mus musculus (Mouse); OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. OX NCBI_TaxID=10090; RN [1] SEQUENCE FROM N.A. RA Miyazaki M., Yamashita T., Taira H., Suzuki A.;

RT "cauxin family protein.";
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL: AB186393; BAD35016.1; -.
 DR GO: GO:0003824; F:catalytic activity; IEA.
 DR InterPro: IPR002018; Carboxylesterase.
 DR pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 575 AA; 64166 MW; 3EB9D85981D9DE0A CRC64;

Query Match 68.0%; Score 2094.5; DB 2; Length 575;
 Best Local Similarity 68.5%; Pred. No. 3e-151;
 Matches 390; Conservative 69; Mismatches 99; Indels 11; Gaps 1;

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QY 12 WCFEFLQPLHGRQMGKTPSAGPQRNTRLGWIQKQVTVLGSPPVNVFLGVFPAP 71
DB 17 WIFGALIE-----GSVTEBPHRYTKLGWVGQKQATVLRLEPVAIVFLGIPFAAP 65
QY 72 PLGSLRFTNPPQASWMDLREATSYPNLCLQNSEMLLDQHLKHYPKFGVSEDCLYN 131
DB 66 PLGPIRFKRPKPFALLMDSRSTRIGLVGKQATVLSGTMVNVFLGIPFAAPPLGPI 125
QY 132 IYAPAHADTSGKLPVLMFPGGAFTGASIFDGSALAAVEDVLVYVYRLGIFGFTT 191
DB 126 IYAPAHADTSGKLPVLMFPGGAFTGASIFDGSALAAVEDVLVYVYRLGIFGFTT 185
QY 192 WDOAHAGMAFKQVALSWYQKNIFFGQDPSVTITGSGAGASVSSLLSPMAKGLF 251
DB 186 QNHAPGNWMAFARTGNPNLWRENIKIFGAGNPSVITFGNSAGASISLISPLSADLF 245
QY 252 HKAIMESGVAIIPYLEAHDEVKESDQLVVAHFCGNNAASDEALRLCTKPKSKELTLIS 311
DB 246 HKAIMESGVAIIPYLEAHDEVKESDQLVVAHFCGNNAASDEALRLCTKPKSKELTLIS 305
QY 312 KTKSFTVVDGAFPPNPPLDLISQKAFAPSIIGVNNHEGFLPMKEAPEILSGNSK 371
DB 306 KAKSFTVVDGAFPPNPPLDLISQKAFAPSIIGVNNHEGFLPMKEAPEILSGNSK 365
QY 372 LALHLIQLNLTIPPQYLHLVANEFYHDKSLTEIRDSLIDLGLGVFPVVPALITARYH 431
DB 366 TALTLHTLHTIPTQHLVYTKVEYFHKGSPTDIRDTLIDLGLGVFPVVPALITARYH 425
QY 432 AGAPVYFEYERHPPQCFEDTKPAFYKADHDEVRFVVGGAFLKGLDYMFGATEEKKLS 491
DB 426 SGGPVYFEYERHPPQCFEDTKPAFYKADHDEVRFVVGGAFLKGLDYMFGATEEKKLS 485
QY 492 RQMKWMAFARTGNPNLWRENIKIFGAGNPSVITFGNSAGASISLISPLSADLF 551
DB 486 RQMKWMAFARTGNPNLWRENIKIFGAGNPSVITFGNSAGASISLISPLSADLF 545
QY 552 ILSASDMLHSPSSITFLSLOPFFFCAP 580
DB 546 ILSASDMLHSPSSITFLSLOPFFFCAP 574

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RESULT 6

Q81034 PRELIMINARY; PRT; 545 AA.

AC Q81034; DT 01-MAR-2003 (T-EMBLrel. 23, Created) DT 01-MAR-2003 (T-EMBLrel. 23, last sequence update) DE Carboxylesterase-like urinary excreted protein. GN Name=cauxin; OS Felis silvestris catus (Cat); OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Carnivora; Fissipedidae; Felidae; Felis. OX NCBI_TaxID=9685; RN [1] SEQUENCE FROM N.A.

RC TISSUE=Kidney; PubMed=12401131; DOI=10.1042/BJ20021446;
RX MEDLINE=22458314; PubMed=12401131; DOI=10.1042/BJ20021446;
RA Miyazaki M., Kamie K., Soeta S., Taira H., Yamashita T.;
RT "Molecular cloning and characterization of a rat carboxylesterase-
RT like protein that is physiologically present at high concentrations in
RT the urine of domestic cats (Felis catus).";
RL Biochem. J. 370:101-110(2003).
CC - - SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; AB045377; BAC2577.1; - -
DR HSSP; P12337; 1K4Y.
DR GO; GO:0016787; P:hydrolyase activity; IEA.
DR InterPro; IPR002018; CarboxesteraseB.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00132; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolyase. 545 AA; 60505 MW; 9F73FA693277FA9 CRC64;
SQ SEQUENCE

Query Match	64.5%	Score 1985;	DB 2;	length 545;
Best Local Similarity	71.7%	Pred. No. 6.5e-143;		
Matches 373;	Conservative 60;	Mismatches 85;	Indels 2;	Gaps 2

Qy	31	GPAEPONTRLGWLOGQVTVLSPVNVNVLGVPAAPLPLSLFTNPOQSPMDNL	90
Db	25	GPADADPVASTRIGMRGKQTTVLASTYFVNMFLOIPIAAPPGLRFKQPKPLPGNDF	84
Qy	91	REATSYPNCLQNSEWLLDQHMULKVHPKFSVEDCYLNIYAPAHADTGSKLPLVMF	150
Db	85	RNATSTFKLCFQDLEBLVSYQHVLKRRPKLEASBDCYLNIYAPAHADNSNLPVMWF	144
Qy	151	PGGAFKTSNASIFDGSALAAVEDVLVVVVQYRLGIFGFPTTWDQHPGNMAFKQVAAIS	210
Db	145	PGGAFKGSASPFSDGSALAAVEDVLIYTTQYRLGIFGFPTDGEHAGNMALLDQVAAIT	204
Qy	211	WYQKQIEFGQDSSSTIRGESAGAISVSSLLTSMAGLPHKAKMESGVIIPIYL-EAH	265
Db	205	WYDNIEFGQDRAVYTIIGESAGAISVSSLLTSLIANGLPHKAKMESGVAILPLMRPP	264
Qy	270	DYKSEDLQVVAHFCCNNASDSBALRLCRTLKPSKELLTLSOKTSPFRVVDGAFPNPE	329
Db	265	GDERKCDLOVLAITCCGSHASDSALLQCLRAKPSSEIMDISKULTFSIPVTDFFPFDER	324
Qy	330	LDELQKAFKALPISIIIGVNNHECGFLPMKEAPBELLSSGNSKSLAHLIQLNIIHPIQYH	389
Db	325	VALLTQKAFNSVPSIIIGVNNHECAFL-STBSEITIGSNSNLSLIYHTEFLNIPQYH	383
Qy	390	LVANEXYFHDKSLTEIRDSLLDLQDVFVVPALITAYRHDAGAPVYFYEFRHRPOCFE	449
Db	384	LVADHYFYNGKSPVEIRDSFLDLQDVLFPVVGAVTAYRHADAGAPVYFYEFGHPCLN	443
Qy	450	DTPAPAFKADHADBEVAFVFGGAPLKGDIYMFEGALTEBEKLSRKMKMYALFATGPNG	509
Db	444	DTPAPAFKADHDSBEIRFVFGGAPLKGDIYMFEGALTEBEKLSRKMKMYANFARTGPNG	503
Qy	510	NDLSIMPAVNLTEOYLOLDLNMISLGORLKEPBYDFTSTI	549
Db	504	EGVPLMPAYIQSQEYKLLDLSVSGKLKEQSEVERFMWNTI	543

RESULT 7	
095KH3	
ID 095KH3	PRELIMINARY; PRT; 361 AA.
AC 095KH3;	
DT 01-DEC-2001 (TrEMBLrel. 19, Created)	
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE Hypothetical protein.	
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;	
OC Cercopithecinae; Macaca.	
NCBI_taxid=9541;	

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Temporal lobe right;
 RA Otsuda N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1-SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL; AB060873; BAB46884.1; -
 DR HSSP; F12337; 1K4Y.
 DR InterPro; IPR002018; CarbesteraseB.
 DR Pfam; PF00135; Coesterase; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 361 AA; 41032 MW; AC62AB6E78C5F1A1 CRC64;

Query Match	54.4%	Score 1676.5	DB 2	Length 361
Best Local Similarity	95.0%	Pred. No. 1,4e-119		
Matches 323, Conservative	5	Mismatches 11	Indels 1	Gaps 1

QY	24	ILSPMKGFHNAIMSGVAILPYLEADYKSESDLOVAHFAFCNNMSDEALLRCJRTK	301
Db	17	ILSPMKEGLFHNAIMSGVAILPYKATDYKSESDLOVAHFAFCNNMSDEEDLLRCJRTK	76
QY	302	PSKELLTTSQTKSFTRVVDGAFPNEDJLLSOKAFALPISIIGVNNHCEGFLLPKEA	361
Db	77	SSKELLTTSQKAKSFTFRVVDGAFPNEDJLLSOKAFALPISIIGVNNHCEGFLLPW-EA	135
QY	362	PEILSSGNSLALHLIQLNIHLIPQYLHVANEXFHDKHSITETIRDSLLDLGDFVFPV	421
Db	136	PEILSSGNSLALHLIQLNIHLIPQYLHVANEXFHDKHSITETIRDSLLDLGDFVFPV	195
QY	422	ALITTAHYHDGAPVYFYEFRRHPOCFEDTYPAPFKADHAEVAFVGGAFLLKDDIYME	481
Db	196	ALITTAHYHDGAPVYFYEFRRHPOCFEDTYPAPFKADHAEVAFVGGAFLLKDDIYME	255
QY	482	GAITEERKLSRKMKMKWATFARTGNPNNDLSIWPANYLTCQYQLDLNMSIGORLKEPR	541
Db	256	GAITEERKLSRKMKMKWATFARTGNPNNDLPMBAINLTCQYQLDLNMSIGORLKEPR	315
QY	542	VDPMWSTIPILSASDMLHSPLSSTLPFLSLQPPFFCAP	581
Db	316	VEPMWSTIPILSASDMLHSPLSSTLPFLSLQPPFFSCVP	355

RESULT 8			
SASB_ANAPL	STANDARD;	PRT;	557 AA.
ID SASB_ANAPL			
AC 004791;			
DT 01-FEB-1995 (Rel. 31, Created)			
DT 01-FEB-1995 (Rel. 31, Last sequence update)			
DT 25-OCT-2004 (Rel. 45, Last annotation update)			
DE Fatty acyl-CoA hydrolase precursor, medium chain (EC 3.1.2.-)			
DE (Thioesterase B).			
OS Anas platyrhynchos (Domestic duck).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Eukaryota; Aves; Neognathae; Anseriformes; Anatidae; Anas.			
OK NCBI_TaxId=8839;			
RM [1]			
RN SEQUENCE FROM N.A., AND SEQUENCE OF 26-65.			
RP TISSUE=Uropygial gland;			
RX MEDLINE=93300823; Pubmed=8314791;			
RA Hwang C.-S., Kolatukudy P.E.;			
RT "Molecular cloning and sequencing of thioesterase B cDNA and			
RT stimulation of expression of the thioesterase B gene associated with			
RT hormonal induction of peroxisome proliferation. ";			
RL J. Biol. Chem. 268:14278-14284(1993).			
-1- FUNCTION: Fatty acid biosynthesis chain termination and release of			
the free fatty acid product is achieved by hydrolysis of the thio			
ester by a thioesterase. This thioesterase may be associated with			
peroxisome proliferation and may play a role in the production of			
3-hydroxy fatty acid diester pheromones.			
-1- TISSUE SPECIFICITY: Highest levels in uropygial gland, much lower			
in liver and kidney.			
-1- SIMILARITY: Belongs to the type-B carboxylate esterase/lipase family.			

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).

DR EMBL: L05493; AAA4923.1; -
 DR PIR: A47162; A47162.
 DR HSSP: O75540; 1K4Y.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR00379; Ser. ester.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR Direct protein sequencing; Fatty acid biosynthesis; Hydrolase; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 557 Fatty acyl-CoA hydrolase.
 FT ACT_SITE 227 227 Acyl-ester intermediate (By similarity).
 FT ACT_SITE 345 345 Charge relay system (By similarity).
 FT ACT_SITE 460 460 Charge relay system (By similarity).
 FT DISULFID 93 122 By similarity.
 FT CARBOHYD 476 476 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 557 AA; 61637 MW; 03E35D90A037FEB0 CRC64; (Potential).

Query Match 42.2%; Score 1298.5; DB 1; Length 557;
 Best Local Similarity 48.4%; Pred. No. 1.9e-90;
 Matches 265; Conservative 79; Mismatches 177; Indels 27; Gaps 8;

QY 30 TGPSAGPQNRRLGHIQKQVTVLGSVPVNVFLGVPEAPPLSLFTNPQAPSPMDN 89
 23 TGKAKQPEVTVYVYGVGVYQVKNVAERSVNVFLGLPFAKPPVPLRFSPPPEPKWG 82
 90 LREATSYNLCIQNSEMLLDQHL-----KHVYKFEVSEDCLYLNYAPAHADTSKL 144
 83 VRDASYPKQDK---VLGQYLSDAITNRKRYRQISBDCLYLVYFVSTEQEKL 139
 145 PVLVWFPGGAFKTSASIFDGSALAYEDLVVVVQVYLGIFGFTTMDHAPNMAFKD 204
 140 PFLVVIHGGGLVSGAASSYDGSALAFNVVVVVIQVRLGAGVFGDHAAGNNGYLD 199
 205 QVALSWYQKNIIEFGDPSVITFGESAGALISVSLISPMAGLPHKAIMESGVAL-1 263
 200 QVALLOWIQENIIRFGDPSVITFGESAGVSVSALVLPKAGLPHKAIMESGVAL-1 259
 264 PYLEAHVYKSEDIQVVAHFCGNASDSEALLRCLFTKPSKEL--LTLSQKTSFTRVVD 321
 260 LFTL-----QPEEQARIAAAGCEKSSSALLVCLARKTAHEQITLTKMPMFIASID 315
 322 GAPPNEPLDLLSQAKFAPSIIGVNNHCGFLP-MKEAPEILSGSNKSLALHLQNI 380
 316 GVFFPKSPRLLSKVNAVPIYIIGVNNCFGILPRMKPFPEFTGLEKQVAVQLGST 375
 381 LHT-----PQVYLAHVANEYFHDKSLTEIRDSLLDLLGVFVYVPAITAYHDAAP 435
 376 LAISFKGAPEDIDVLVYNEYIYGAENRAQVROGLDSDIDPFLVSAEVAAHHRDAAP 435
 436 VYFVFEHRPQCEPDITKPAFVADADDEVYFVFGAFLKGDITMEGATEEKLISRRM 495
 436 VYFVFEHRPQCEPDITKPAFVADADDEVYFVFGAFLKGDITMEGATEEKLISRRM 495
 496 KTWATFARTGNPNDLSLMPAVNLTEOYLQDLMLMSLQGLKPKPRVDFTSTPLISA 555
 490 KWTNVAARNGNPNEGELVHMPQYDMDERLEIDLTQKAKKLKPKRMEFWMLTQEI 549
 QY 556 SMLTSP 563
 Db 550 RRRKHTDL 557

Q91WGO ID Q91WGO PRELIMINARY; PRT; 561 AA.
 AC Q91WGO; 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
 DE Carboxylesterase 2 (Carboxylesterase M13 precursor).
 CN Name=Ces2; Synonyms=cee2a3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon, and Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Ffrench J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalske U., Smallus D.B., Schmech A., Schlein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Kidney;
 RX Strausberg R.;
 RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX Strausberg R.;
 RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX Strausberg R.;
 RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon, and Kidney;
 RX Strausberg R.;
 RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Liver;
 RX MEDLINE=22744052; PubMed=12859986; DOI=10.1016/S0003-9661(03)00286-8;
 RA Furuhata T., Hosokawa M., Nakata F., Satoh T., Chiba K.;
 RT "Purification, molecular cloning, and functional expression of
 inducible mouse liver acylcarnitine hydrolase in C57BL/6 mouse,
 belonging to the carboxylesterase multigene family".
 RL Arch. Biochem. Biophys. 416:101-109(2003).
 CC "1- STIMULATED: Belongs to the type-B carboxylesterase/lipase family.
 EMBL: BC015290; AAH15290.1; -
 EMBL: BC024552; AAH24552.1; -
 EMBL: BC031170; AAH31170.1; -
 EMBL: BC034178; AAH34178.1; -
 EMBL: BC034180; AAH34180.1; -
 EMBL: BC034191; AAH34191.1; -
 EMBL: AB110073; BAC76623.1; -

RESULT 9

DR HSP, P12337, 1k4Y.
 DR MGD; MGI:2385905; Cee2.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYL ESTERASE B_1; 1.
 DR PROSITE; PS00941; CARBOXYL ESTERASE B_2; 1.
 DR Hydrolyase; Signal.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 561 carboxylesterase M13.
 SO SEQUENCE 561 AA; 62469 MW; F793967A646EB728 CRC64;
 Query Match 41.7%; Score 1282.5; DB 2; Length 561;
 Best Local Similarity 48.4%; Pred. No. 3.2e-89;
 Matches 276; Conservative 77; Mismatches 174; Indels 43; Gaps 14;

14 FLLIOPLLGHOMGTGSPASGAPORNTLGMIOGQVAVLSPVAVNVLGVPAAPL 73
 15 FELL--LIIHVQ--GODSPEA--NPIRNTTGOIQSLIVKDTKAGVHTFLGIPFAKPV 70
 74 GSLRFTNPQAPSPMDLREATSYPLNCLONSEML-----LLDQMLKVHYKGVSEDCLY 129
 71 GLRFAPAPAPAPSPGVRDGTAPAMCQNLMDLMDNAGLPDKMKMLSSFP--MSDCLY 127
 130 LNIYPAHAADTSGKLPVLPVFGAGFKTSASIFDGSALAAVEDLVVVVYRLIGFGRF 189
 128 LNIYTPAHMEGSNLPVWVWVINGALVIGMAGMFDGSLTVNEDLVVVTIQYRLGVLPF 187
 190 TTMDDHAPNNAPKQOVALSWQKNIIEFGGDPSPSVTFGSSAGASVSSLSLPMAG 249
 188 STGDDHARKNMGYLDQAAALRWQOINAFGSGNPDRTVTFGSSAGTSVSSHVSMSG 247
 250 LFHKAIMESGVAIIPLEAHNDEKSEDLQ--VVAHFCGNASDEALRLCRTPKSKELT 308
 248 LFHGAIMESGVALLPPLIS--ETSMVSTYAKLSGCGAMSOALVRLRGSEAEILA 304
 309 LSQKTKSFTRVVDGAFEPNEPDLISQKPKAIPTITGVNNECGCLLMKEAPELSS 368
 305 INKVFPMIPAVVDGEFFPHPKELLASEDFHVPVSIIGVNDGFGWISIP-----VWGS 358
 369 N---KSLMLHLONLH-----IPROYLHVANVYFPHDKSLYEIRSLDLGDPVF 418
 359 AQMIGITRENIQAVLKDTAVQOMLPPECSDLMEYMGDTEDAQTLQIQFTMEGDMF 418
 419 VVPALITARYHDAGAPVYFEFRHRPQCFEDTKPAFVADHADEVYFVGCAF--LKGD 476
 419 VLPALQVAHFOR--SHAPYFYEFGHPSYKQVPRPHVADADDELFPYFAEFPMKUD 477
 477 IVMFEGATEEKKLSRKMKYWATFARTGNPNGNDSLMPAYNLTEQYQLDNLNSLGR 536
 478 F-----TEEBELSRBMKYWANFARHGNPNSEGLPYVPVMDHDEQYQLDIIQPAVGRA 531
 537 LKEPRVDFWTSTIP---LLISASDMLHSL 563
 532 LKAGRLQFWTKTLPKRIQELKASQDKREL 561

RESULT 10
 Q8BK48 PRELIMINARY; PRT; 559 AA.
 AC Q8BK48; 01-MAR-2003 (Tremblrel, 23, Created)
 DT 01-MAR-2003 (Tremblrel, 23, last sequence update)
 DT 05-JUL-2004 (Tremblrel, 27, last annotation update)
 DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
 DE RIKEN full-length enriched library, clone:5031415B19 product:similar
 DE to CARBOXYL ESTERASE (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE)
 DE (MONOBUVYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE)
 DE (9030624102RIK; (9030624102RIK;
 GN Name=9030624102RIK;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Yumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwaigi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
 RA Adachi J., Aizawa K., Akiyama T., Aikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kanakawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsumoto T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sato H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takawa-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RT Submitted (Apr-2002) to the EMBL/Genbank/DBD databases.
 RL [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold F.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Uedin T.B., Tishiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggheffano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richardes S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywniaki M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.,
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL; AK077248; BAC36707.1; -;
 DR EMBL; BC055062; AAH55062.1; -;
 DR HSSP; P12337; IK4Y.
 DR MGI; MGI:2443170; 9030624I02Rik.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR002018; CarboxylesteraseB.
 DR InterPro; IPR000379; Ser_estrB.
 DR Pfam; PF00135; Coesterase_1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolyase.
 SQ SEQUENCE 559 AA; 62317 MW; CC14C61034A122C3 CRC64;

Query Match 41.6%; Score 1281; DB 2; Length 559;
 Best Local Similarity 48.7%; Pred. No. 4.2e-89;
 Matches 260; Conservative 79; Mismatches 165; Indels 30; Gaps 8;
 QY 31 GGAAGGQNTLRIGTQKQVTVLGSPPVNVFLGPPFAPPLGSLRTNQPSVNDL 90
 DB 26 GQDSAPRINTHTGQVRSGLVHYKDTDLAVHTFLGIPAKPVPVGLRPAPEAPEPESGV 85
 QY 91 REATSYPNCLQNSEWL-LLDQMLKVHPKFGVSEDCLYINITYAPAHADTGSCLPV 149
 DB 86 RGTGTHPMKCLQNDMLMGSEDLKMMNLILPISMSEDCLYINITYAPAHAGSNLPV 145
 QY 150 FFGAFAFKTGSASIFDGSALAAVEDLVVVOYRIGFGFTTMOQHAPGNWAFKQV 209
 DB 146 IHGGLALVGMASMYDGSMLAATEDVVAIYRIGVGIFSTGQHAQKGMWGLDQV 205
 QY 210 SWQGNIEFFGGDPSVTIFGESAGAISVSSLISPMAGLFFKAIMESGVAIIIPYLEAH 269
 DB 206 RMVQGNITHFQGNEDRVYTFEGESAGTSVSSHVS PMSQGLFPGALMESGVAVLPDLIS 265
 QY 270 DYKESDQVVAHFQGNNASDSEALLRCLRTKPSKELLTISQTKSFTFVVDGAFPPNEP 329
 DB 266 SSEWVH--RIYANLSGCAVNSEITLMCCCLGKNAEMLANKVFKIIPGVNGEFLPKRP 323
 QY 330 LDLSQAFAPALPSIIGVNNHCGFLP-----MKEAPEILSGSKSLAHL 376
 DB 324 QELMASDFFPVSIIIGINNDYGMILPTIMPAQKIEITRKTLPVAVL-----KSTALKM 379
 QY 377 IQNLIHLPPQYLHLVANEYFHDGSLTEIRDSLDDLDGVFFVVDALITARYHDAGAPV 436
 DB 380 M-----LPREGCDLMEETVGTDEPETIQAOFRKMGDFMEVLPALQVAFHQR-SHAPV 433
 QY 437 YVEFRRHQCEPDTPAFVAKADHADEVAFVFGAFLKGDIVMFGATEEKKLSRGMK 496
 DB 434 YVEFRRHQCEPDTPAFVAKADHADEVAFVFGAFLKGDIVMFGATEEKKLSRGMK 496
 QY 497 YVATFARTGNPNGLSLMPAYNLTEOYLQDLNMSLQRLKEPRVDFWTSTP 550
 DB 490 YVANFARHGNPNSEGLPYMPVWHDHDEYLDIDIPSGVGRALKARLQFWTKTLP 543

RESULT 11
 035533

ID 035533 PRELIMINARY; PRT; 559 AA.
 AC 035533;
 DT 01-JAN-1998 (TrEMBLrel. 05. Created)
 DT 01-JAN-1998 (TrEMBLrel. 05. Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26. Last annotation update)
 DE Carboxylesterase precursor (EC 3.1.1.1).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Syrian golden; TISSUE=Liver;
 RA Some T., Wang C.Y.,
 RT "Microsomal amidases and carboxylesterases.",
 RL (In) Guengerich F.P. (eds.)
 RL COMPREHENSIVE TOXICOLOGY VOLUME 3, Biotransformation, pp.265-281,
 RN Pergamon, Oxford (1997).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Syrian golden; TISSUE=Liver;
 RA Some T., Ishida Y., Takabatake E., Wang C., Isebe M.,
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL; D50577; BAA23605.1; -;
 DR HSSP; P12337; IK4Y.
 DR GO; GO:0004091; F:carboxylesterase activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR InterPro; IPR002018; CarboxylesteraseB.
 DR InterPro; IPR000886; ER_target_S.
 DR InterPro; IPR000379; Ser_estrB.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolyase; Signal.
 FT SIGNAL 1 27 Potential.
 FT CHAIN 28 559 carboxylesterase.
 SQ SEQUENCE 559 AA; 62126 MW; 5B6BD4F9A47C6AD8 CRC64;

Query Match 41.5%; Score 1276.5; DB 2; Length 559;
 Best Local Similarity 49.6%; Pred. No. 9.2e-89;
 Matches 262; Conservative 79; Mismatches 172; Indels 15; Gaps 9;
 QY 28 GKTGSAAGPQNTLRIGTQKQVTVLGSPPVNVFLGPPFAPPLGSLRTNQPSV 87
 DB 26 GQDSAPRINTHTGQVRSGLVHYKDTDLAVHTFLGIPAKPVPVGLRPAPEAPEPESGV 82
 QY 88 DNRREATSYPNCLQNSEWL-LD-QHMLKVHPKFGVSEDCLYINITYAPAHADTGSCLPV 146
 DB 83 SGVRDGNSTFPMKCLQNDMLMGSEDLKMMNLILPISMSEDCLYINITYAPAHAGSNLPV 142
 QY 147 LWFPGAFKTSASIFDGSALAAVEDLVVVOYRIGFGFTTMOQHAPGNWAFKQV 206
 DB 143 IHGGLALVGMASMYDGSMLAATEDVVAIYRIGVGIFSTGQHAQKGMWGLDQV 202
 QY 207 AALSWQGNIEFFGGDPSVTIFGESAGAISVSSLISPMAGLFFKAIMESGVAIIIPYLEAH 266
 DB 203 AALRWQGNITHFQGNEDRVYTFEGESAGTSVSSHVS PMSQGLFPGALMESGVAVLPDLIS 262
 QY 267 EANDYKESDQVVAHFQGNNASDSEALLRCLRTKPSKELLTISQTKSFTFVVDGAFPP 326
 DB 263 ISSSEWVH--YTIYANLSDCAVNSEITLMCCCLGKNAEMLANKVFKIIPGVNGEFLPKRP 320
 QY 327 NEPLDLSQAFAPALPSIIGVNNHCGFLP-----MKEAPEILSGSKSLAHL 382
 DB 321 KHPQELLASADFFPVSIIIGINNDYGMILPTIMPAQKIEITRKTLPVAVL-----KSTALKM 380
 QY 383 IPPQYLHLVANEYFHDGSLTEIRDSLDDLDGVFFVVDALITARYHDAGAPV 442
 DB 381 LPREGCDLMEETVGTDEPETIQAOFRKMGDFMEVLPALQVAFHQR-AHAPVYFVFGQ 439
 QY 443 HRQCEPDTPAFVAKADHADEVAFVFGAFLKGDIVMFGATEEKKLSRGMK 502

DB 440 HRPSPFKDTRPHRYVAKDHGDEFFEVGNG-LLCG--IKF-ASTEEBELSRKMKYANFA 495

Qy 503 RTGPNPNDLSLWPAVNLTEQYIQDLNLSGRLKEPRVDFTSTIP 550
496 RAGNPENSENLPYPMMDHDEQYQDLIDKPAVGRALAKARLRQFTWTKLIP 543

Db

RESULT 12

Q8BM97 ID Q8BM97 PRELIMINARY; PRT; 559 AA.

AC Q8BM97;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030624l02 product:similar to CARBOXYL ESTERASE (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE). (PROCAINE ESTERASE) (METHYLBUTYRASE).
DE Name:9030624L02R1K;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=92979253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RA The FANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team,
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komio H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.153600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Komio H., Akiyama Y., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplexed capillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Query	Match	Local Similarity	Score	Length
Db	31	65AAGPGQRYRTRLMGIGQKQVTVLGSFVPPVNFGLVFPAPPLGLSFFPTNPQAPSPMDNL	41.3%	559
Qy	26	QGSASISRNTHHNGQVAGSLVHVMDTDAVHTFLGIFPAKRPVPLRPAPEADEPMGCV	48.7%	88
Db	91	REATSYNCLONSFWL-LDDHMLKXHYKFGVSECLTYNTIAPAHADGSLPLVLM	76	166
Qy	86	RDGSHPNMCLQNDNLMGSEDLKMMNLILPISMSBCLTYNTIYVPAHAGSNLPVWVV	166	30
Db	150	PPGCAFPTGASLFPDGSALAAEDVLVWVQYRLGIGFPTTMDQAHGNNAPFDQVAA	166	30
Qy	146	THGALTVGASMSWDGSMLANTEDEVVVAIQYRLGVGFSTGQAHKMGVLDQVAA	166	30
Db	210	SWVQKNIEFGGDPSSVTIFGESAGAISVESLILSPNAKGLFHKAINESGVALIPYLEAH	166	30
Qy	206	RMVQGNLVHNGANDRTIIFGESAGISVSHSVSPMSQGLFHAINESGVALIPDLISS	166	30
Db	270	DYKESDLOVVAHFCGNNASDSEALLRCLRTKPSKELLTLISQKTSFTRVVDGAFPPNEP	166	30
Qy	266	SSEWVH--RIVANLSGCAAVNSELMCLCGKNEAEMLAINKVKKIIPGVVDGFEFLPHP	166	30
Db	330	LDLISQAFKAIPIBITGVNNHECGFLRP-----MKAPRILISGNSKSLAHL	166	30
Qy	324	QELMASDFHPVPSIIIGINDDEGWMILPTMDPAQKIEITRKLPLPVL---KSTALKM	166	30
Db	377	IONLHPIPOYLHVANVEYFHDKSLTEIRDSLLDLGLGVFVVPAALITARYHRDAGPV	166	30
Qy	380	M-----LPPEGGLIMEEYMGDTBEDPTLQAQPFEMGDMFVFVPLAQVAFHQR-SHAPV	166	30
Db	437	YFYEFRHRPOCFEDTKPAFYKADHADEVRFVFGAGFLKGLDIWMFEGATEEBSKLISRKMK	166	30
Qy	434	YFYEFGHRPSPFQFRPPYKADHGEDEIFLVFGYQF--GNIKL--PYTEEBEQLSRMMK	166	30
Db	497	YMATPATTGNPNNGDLSLMPAYNLTEOYLQDLNMSLGGQRKERVDFWFTSTIP	166	30
Qy	490	YRANFAHGNPNSEGLPYWPMVDHDEQYLDLDIOPSVGRALKARRLOFWTKTLP	166	30

GN Name=BC015286;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=10090;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettelman M., Madan A., Young A.C., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/1ipase family.
 DR EMBL; BC058815; AAH58815.1; -
 DR HSSP; P12337; 1K4Y.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000379; Ser_catalase.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 DR Hydrolase; Hypothetical protein.
 KW
 SQ SEQUENCE 556 AA; 61927 MW; 58DE05A3C73BECD CRC64;
 Query Match 41.1%; Score 1266.5; DB 2; Length 556;
 Best Local Similarity 47.1%; Pred. No. 5.3e-88;
 Matches 273; Conservative 76; Mismatches 190; Indels 41; Gaps 12;
 QY 1 MPQGLTSSASQWCFLL--LQPLIGRQMGKTPSAEGQRNTRIGLQKQVTVLGSPPV 58
 DB 1 MPR---SQMNHWLDVLLFGLLLLLVHVG-QQDSPEA-SPIRNTHTGQVAGSLVHKDTKA 55
 QY PVNVFLGVPPRAAPPLGSLRFTNPQAPSPMDNIREATSPNLCLONSWMLLDQMLKXHY 118
 DB 56 GYHTFLGIPPAKPPVGPRLRPAPEAPEPWSGVGDGTAHPAMCLQ-----LGMKEIKKL 111
 QY 119 PKGVSEDCLYNINIVAPAHADTGSKLPLVWFPFGAFTGSASTPDGALAAVEDLVVV 178
 DB 112 PAVSTSEDCLYNINIVAPAHAGSNLPLVWVTHGGGLVAGMASWYDGLAAILIDLVVVT 171
 QY 179 VQYRLGIRFGEFTTQOAHAGNAPFDQVAAISWQKNEFFGSGPSSVTIFGSSAGASIV 238
 DB 172 IQYRLGVLEFSTGQOHAGNMGFLDQVAAALRWIQONIAHCGKPRDVTTFGSSAGGTSV 231
 QY 239 SSLISPAKGLFHAIMESGVAIIPYLEADHYEKSELDQVVAHFCCNNASDSEALLRCL 298
 DB 232 SSHVVSPPMSKGLFHAIMESGVALIPYITDTSMS--TTVAALSGCEAMSEALVRCI 289
 QY 299 RTKPSKELLTSQKTKSTRVVDGAFFPNEBLLDLSQAKFAKLPSTIIGVNNHCGSLWM 358
 DB 290 RGSBAELTALAKLVQMIPAVVDEFPFPRHPKELLASEDBHPVPSIIGVNNDEFGWITP- 348

QY 359 KEAFITSGNSKSLALHLQNI-----LHIPQYLIHVAHYFHDKSLTREIRDS 408
 DB 349 -----VWWSAQTIKEITRENLQAVLKNNTAQMLPPEBCDILMEYWDTEDAQTLLQ 403
 QY 409 LLDLIGVFPVPLILTAARHDAQAPVYFEFRHAPQCFEDTKPAFYKADHAEVRFV 468
 DB 404 FTEWMEFMTVITPALOVAYFQR-SHASVYFEFHQIADLKQVRPTHKADHADIPIVF 462
 QY 469 GGAF-LKGDIVMEGATEEEKLSRQMKRYATFARGNPNGNLSLWPAVNLTEQYLO 526
 DB 463 GYFPMWDKDPF-----TEGEKLSRMMKYANPAKRGNSBGLPWPVMDHDEQYLQ 516
 QY 527 LDINMSIGRLKRPVDFPTSTIP---LILASDMLHSP 563
 DB 517 LDQPAVGALSRRLQFWTKLSQKIQELRASQDKTEL 556
 RESULT 14
 ID OEGM54 PRELIMINARY; PRT; 568 AA.
 AC OEGM54;
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DE LOC443703 protein (Fragment).
 GN Name=LOC443703;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettelman M., Madan A., Young A.C., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Fontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 Dev. Dyn. 225:384-391(2002).
 RL
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/1ipase family.
 DR EMBL; BC074230; AAH74230.1; -
 DR GO; GO:0016787; F:hydrolase activity; IEA.

DR InterPro: IPR002018; CarboxylesteraseB.
 DR InterPro: IPR000379; Ser_estr.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 KM Hydrolyase.
 FT NON_TER
 SQ SEQUENCE 568 AA; 63032 MW; 93360B6B53931A1 CRC64;

Query Match 41.0%; Score 1263.5; DB 2; Length 568;
 Best Local Similarity 48.2%; Pred. No. 9.2e-88;
 Matches 258; Conservative 87; Mismatches 169; Indels 21; Gaps 8;

QY 28 GKTGSAEGPQNRTRIGWIGQKQTVLGSPPVNVFLGPPAAPPLGSLRFTNPQSPW 87
 DB 28 GYGVEDARPLLTITVYGGILGKTVGAKETDRLIHFMGVPAKPRIGLRFEDPOPEBW 87
 QY 88 DNLRATSPNLCIONSEWL--LLDQHLKHYPRFGVSEDCLYNITVAPAHADTGSKL 145
 DB 88 SSIRREATERPMLCDKKGMEQLADFPKAKPDP--VSEDCLYNITVTPADRGENPELP 145
 QY 146 VLVMPFGGAFKTSASIFDGSALAYEDLVVVVQYRIGI RGFPTTWDHARGNAFKDQ 205
 DB 146 VNVFTHGGGLTGMGAMFEGSALSAVENVVSIGRLGIMGFSTGDKEAKGNYGFLDQ 205
 QY 206 VVALSMVQKNIEFGGDPSSVTITFGESAGAISSSLISPMAGLPHKAIMESGVALIPY 265
 DB 206 VVALMKNVDNIDKPGNPGSVITIFGESAGLSVSAQVLSPLSKGLFHRALISSGVALIPG 265
 QY 266 LEADHSESDIQVVAHFPGNNASDS--EALLRCLRTKPSKELLTYSQTKT--SFTRVVDG 322
 DB 266 LMA---SKTEKILPIHVAANTSSCSVSLADCLKKTEDEIVAI SAAMKFAVFAVVDG 322
 QY 323 APPHEPDLDSQAFKAPSIIGVNNHCGFLPMPKEAPELLSGNSKSLALHLIONILH 382
 DB 323 VFLPRAEELIASKSNPVPFLIGVNNHFGWILPALN--ISGRHEMEKDDIOSILV 379
 QY 383 IPPQYLH-----LVANEYFHDKSLTEIRDSLLDLGDFVFPVVALITARYHDAAP 435
 DB 380 ALP-FVHSTSVVPIMEYFGDTNDPKLRNNPFDLVGDIIIFVLPALATARYHDSGR 438
 QY 436 VYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGAFELKGDIVMEGATEEBSKLSRKM 495
 DB 439 VYFYEFGHRPSMYDKODPFVADHDDELIFVVGGFPLKSGILFKSNGTEBSKLSKTM 498
 QY 496 KYMAFPARTGNNGNDLSMPAYNLTEOYLQDLNMSLQGLRKERVVDWTSTIP 550
 DB 499 KYMANFARNGDNGGLAEMPRYDEDEYLEIKLTQESSQRLKGGRFKFWTTL 553

RESULT 15

ID 070177 PRELIMINARY; PRT; 561 AA.
 AC 070177;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Carboxylesterase precursor (EC 3.1.1.1).
 GN Name=carboxylesterase;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Miscar; TISSUE=Small intestine;
 RA Sone T., Kunikomo T., Isebe M.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY. Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL: AB010632; BAA25691.1; -.
 DR HSSP: P37967; I0E3.
 DR GO: GO:0004091; F:carboxylesterase activity; IEA.
 DR GO: GO:0016787; F:hydrolyase activity; IEA.

DR InterPro: IPR002018; CarboxylesteraseB.
 DR InterPro: IPR000379; Ser_estr.
 DR Pfam: PF00135; Coesterase; 1.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 KM Hydrolyase; Signal.
 FT SIGNAL
 FT CHAIN 1 26 Potential.
 FT CHAIN 27 561 carboxylesterase.
 SQ SEQUENCE 561 AA; 62239 MW; 73A468C3F96939B CRC64;

Query Match 41.0%; Score 1262.5; DB 2; Length 561;
 Best Local Similarity 48.8%; Pred. No. 1.1e-87;
 Matches 275; Conservative 77; Mismatches 179; Indels 33; Gaps 13;

QY 1 MPOG-LTSSAQWCFLLIQLPLGHRQKTPSAEGQRTYRLGWIQKQTVLGSPPV 59
 DB 1 MPRNQLHMLNANVLFGLL--LLIHVQ--GQSSPS--SIRRTHTGQVQKLDHVDYTAG 56
 QY 60 VNVFLGVPPAAPPLGSLRFTNPQSPVNDLREATSYNLCIONSEWL--LLDQHLK 115
 DB 57 VHTFLGIPFAKPPVPLRFAPPEPEPPEPWSGVADATSOAMCQIONDIIDEVGLDMKMI- 115
 QY 116 VHYPRFGVSEDCLYNITVAPAHADTGSKLPLYVMPFGGAFKTSASIFDGSALAYEDLV 175
 DB 116 --LSSISMSSEDCLYNITVAPAHAREGSLPVWVWTHGALLVGMASMTDGLITVNEIDL 173
 QY 176 VVVVQYRIGIFGFPTTWDHARGNAFKDQVAAALSMVQKNIEFGGDPSSVTITFGESAGA 235
 DB 174 VVTIYRIGVGLGFSTGDEHARGNMGVLDQVALLRMVQONLHFGNINRVTIIFESAGG 233
 QY 236 ISVSSSLISPMAGLPHKAIMESGVALIPLYEADHSESDIQ--VVAHFPGNNASDSAL 294
 DB 234 TSVSHTVSPMSQGLFHGAIMESGVALLPDLIS--ETSEVTSTVAKLSGCEANDSEAL 290
 QY 235 LRCLRTKPSKELLTYSQTKSTRVVDGAFPPNEPDLDSQAFKAPSIIGVNNHCGFL 354
 DB 291 VRCLRAKSGAELIVNKVFKMI PAVVDEFLPRHPEKELLASEDFHPVPSIIIGNTDEYCC 350
 QY 355 LLPM-----KEAPELISGNSKSLALHLIONILHIPQYLHLVANEYFHDKSLTEIR 406
 DB 351 TIRPMVGTQAIKE-----LSRENLAVALKDTAAQMLPPEGCDLLMEBYMGNTDSSQTLQ 406
 QY 407 DSLDLGDFVFPVVALITARYHDAAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRF 466
 DB 407 IQYTEMGDPLFVIBALQVAHFQR--SHAPVYFYEFOHAPSYFKVNRPPHYKADHADEVRF 465
 QY 467 VFGAFELKGDIVMEGATEEBSKLSRKMKYMATARTGNPNNDLSMPAYNLTEOYLQ 526
 DB 466 VF-GSFPFGMKLDF--TEEBRLSRRMKYMANFARQGNPSEGLPYMPALDHDEOYLQ 521

QY 527 LDNMSLQGLRKERVVDWTSTIP 550
 DB 522 LDTHPAVDALAKARRLOFWTKTL 545

Search completed: June 16, 2005, 20:44:57
 Job time : 183 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2005, 20:31:14 ; Search time 42 Seconds
(without alignments)
1032.645 Million cell updates/sec

Title: US-10-674-636-2
Perfect score: 3079
Sequence: 1 MPQGLTSSASQWCFLLIOP.....PLSLTFLSLIOLPPFFFCAP 581

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3079	100.0	581	4	US-10-023-515-2
2	1230	39.9	559	4	US-09-595-682B-28
3	1230	39.9	559	4	US-09-949-016-6426
4	1230	39.9	577	4	US-09-949-016-9670
5	1150.5	37.4	565	4	US-09-595-682B-21
6	1138.5	37.0	566	3	US-09-264-737-2
7	1130.5	36.7	543	4	US-09-595-682B-26
8	1091.5	35.4	584	4	US-08-845-295A-2
9	1091.5	35.4	584	3	US-09-146-933-2
10	1091.5	35.4	584	3	US-09-146-933-2
11	1091.5	35.4	584	3	US-09-150-515-2
12	1034.5	33.6	539	3	US-09-264-737-1
13	942.5	30.6	454	3	US-08-446-100-26
14	942.5	30.6	454	3	US-08-446-100-28
15	942.5	30.6	454	3	US-08-446-100-30
16	942.5	30.6	454	3	US-08-446-100-31
17	940.5	30.5	454	3	US-08-446-100-27
18	940.5	30.5	454	3	US-08-446-100-29
19	871	28.3	574	4	US-10-023-515-4
20	793	25.8	933	4	US-09-949-016-8386
21	786	25.5	823	4	US-09-949-016-6888
22	782	25.4	953	4	US-09-949-016-8387
23	777.5	25.3	843	4	US-09-491-356C-20
24	777	25.2	575	1	US-08-348-920-1
25	775	25.2	823	4	US-09-491-356C-23
26	774	25.1	575	1	US-08-348-920-2
27	772	25.1	848	4	US-09-491-356C-22

28	769	25.0	836	4	US-09-491-356C-21	Sequence 21, Appl
29	765.5	24.9	614	3	US-08-446-100-25	Sequence 25, Appl
30	764.5	24.8	614	1	US-07-732-962A-2	Sequence 2, Appl
31	764.5	24.8	614	2	US-08-370-156-2	Sequence 2, Appl
32	764.5	24.8	614	3	US-08-446-100-19	Sequence 19, Appl
33	764.5	24.8	614	3	US-08-446-100-21	Sequence 21, Appl
34	764.5	24.8	614	3	US-08-814-095-2	Sequence 2, Appl
35	764.5	24.8	614	5	PCT-US92-06106-2	Sequence 2, Appl
36	764.5	24.8	645	4	US-09-949-016-7063	Sequence 7063, Ap
37	764.5	24.8	645	4	US-09-949-016-7064	Sequence 7064, Ap
38	762.5	24.8	614	3	US-08-446-100-20	Sequence 20, Appl
39	761.5	24.7	614	3	US-08-446-100-23	Sequence 23, Appl
40	760.5	24.7	614	3	US-08-446-100-22	Sequence 22, Appl
41	759.5	24.7	600	2	US-08-370-156-4	Sequence 4, Appl
42	759.5	24.7	600	3	US-08-814-095-4	Sequence 4, Appl
43	759.5	24.7	600	3	US-08-975-084-1	Sequence 1, Appl
44	755.5	24.5	617	2	US-08-370-156-6	Sequence 6, Appl
45	755.5	24.5	617	3	US-08-814-095-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-023-515-2
; Sequence 2, Application US/10023515
; Patent No. 6664091
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Slioc-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYL ESTERASE
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023, 515
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-515-2

Query Match	100.0%;	Score 3079;	DB 4;	Length 581;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 581;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MPQGLTSSASQWCFLLIOPLLGHROWKTPSASGPOBNRLGMIQKQVTVGSPVPV	60	
DB	1	MPQGLTSSASQWCFLLIOPLLGHROWKTPSASGPOBNRLGMIQKQVTVGSPVPV	60	
QY	61	NVFLGVPPAAPPLGSLFTNPQPASPMWNLREATSYNLCIONSEWLLDQMLKVHPK	120	
DB	61	NVFLGVPPAAPPLGSLFTNPQPASPMWNLREATSYNLCIONSEWLLDQMLKVHPK	120	
QY	121	FGVSEDCIYNIYVPAHADTGSKLPLVWPFGAFKFGSASIFPGSALAAVEDLVVVVQ	180	
DB	121	FGVSEDCIYNIYVPAHADTGSKLPLVWPFGAFKFGSASIFPGSALAAVEDLVVVVQ	180	
QY	181	YRLGIPFPTTWDHAGPNAFKQVVALSVQKNIEFPQSDPSVTIFGSSAGASVSS	240	
DB	181	YRLGIPFPTTWDHAGPNAFKQVVALSVQKNIEFPQSDPSVTIFGSSAGASVSS	240	
QY	241	LILSPMAKGLFHKAKIMESGVALIIFYLEAHDEKSEDDQVAHFCGNNASDEALLRCURT	300	
DB	241	LILSPMAKGLFHKAKIMESGVALIIFYLEAHDEKSEDDQVAHFCGNNASDEALLRCURT	300	
QY	301	KPSSELLTLOSXTKSFTRVVDGAFPNEDDLLSQKAFKALPSIITGVNHECGFLPMKE	360	

Db 301 KPSKELTLSQKTSFTRVVDGAFPEBPDLLSOKAFKAPSIIGVNHCGFLPKE 360
 Qy 361 APETLSSGNSKSLAHLIQLIHLIPQYLHLVANEYFHDKSLTEIRDSLLDLGDVFPV 420
 Db 361 APETLSSGNSKSLAHLIQLIHLIPQYLHLVANEYFHDKSLTEIRDSLLDLGDVFPV 420
 Qy 421 PALITARYHRGAGPVYEFERHRCPOCEEDTKPAFYKADHADVRFVFGAFLKGDIVMF 480
 Db 421 PALITARYHRGAGPVYEFERHRCPOCEEDTKPAFYKADHADVRFVFGAFLKGDIVMF 480
 Qy 481 EGATEEKLISRKKMKYATFARTGNPNNDLSLMPAYNLTEOYLQDLNMSLQRLKEP 540
 Db 481 EGATEEKLISRKKMKYATFARTGNPNNDLSLMPAYNLTEOYLQDLNMSLQRLKEP 540
 Qy 541 RYDFMTSTIPLIISASDMLHSLSITFSLLOPFFFCAP 581
 Db 541 RYDFMTSTIPLIISASDMLHSLSITFSLLOPFFFCAP 581

RESULT 2
 US-09-595-682B-28
 / Sequence 28, Application US/09595682B
 / Patent No. 6800483
 / GENERAL INFORMATION:
 / APPLICANT: Danke, Mary K.
 / APPLICANT: Potter, Philip M.
 / APPLICANT: Houghton, Peter J.
 / TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of
 / FILE REFERENCE: SJ-0005
 / CURRENT APPLICATION NUMBER: US/09/595,682B
 / PRIOR FILING DATE: 2000-01-16
 / PRIOR APPLICATION NUMBER: 60/075,258
 / PRIOR FILING DATE: 1998-02-19
 / PRIOR APPLICATION NUMBER: PCR/US99/03171
 / NUMBER OF SEQ ID NOS: 30
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 28
 / LENGTH: 559
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-09-595-682B-28

Query Match 39.9%; Score 1230; DB 4; Length 559;
 Best Local Similarity 46.7%; Pred. No. 4.8e-125;
 Matches 248; Conservative 91; Mismatches 168; Indels 24; Gaps 8;
 Qy 31 GPSAEGPQNTRLGMIQKQVTVLGSVPVNVFLGVFPAPPLGSLRFTNPQASPMWDL 90
 Db 26 GQDSASPIRTTHGQVLSLVHVKGANAGVQTFGLGIPFAKPLGLRFAPEPPESMGV 85
 Qy 91 REATSYENLCLQN-----SEWLLDQMLKVHPKRGVSEDCLYINITYAPAHADTGSKL 145
 Db 86 RDGTHPACLODLTAVESEFL-----SQPNMTFSPDSMEDCLYISTTPAHSHSGSNLP 141
 Qy 146 VLVWFGGAFKTSASIFDGSALAAVEDLVVVVVOYRGLIGFTFTWQOHPGNWAFDQ 205
 Db 142 VVWVINGGLVVGMSLVDSMLALENVVVYIIYRLGVIGFSTGDKHATGMWGYLDQ 201
 Qy 206 VVALSVQKNIIEFGGDPSSVTIFGESAGATSVSLISLSPAKGLFKAHAIWESGVAII 265
 Db 202 VVALSVQKNIIEFGGDPSSVTIFGESAGATSVSLISLSPAKGLFKAHAIWESGVAII 265
 Qy 266 LEAHYKSEDI--OVVAHFCGNNADEBALRLCLRTSPSKELLTTSOKTSFTRVVDGA 323
 Db 266 LIA-----SSADVISTVAVNLACQDVDEBALVGCIRKSGKEIILAIKPKFMIPGVVDG 317
 Qy 324 FFPNEPDLISOKAFKAPSIIGVNHCGFLP-----MKAPBILSGNSKSLAHLIQL 379
 Db 318 FLPRHPQELASADQAPVPSIVGNNEFGWILPKWRIYDTQKEMREASQAALQKMLT 377
 Qy 380 ILHLPQYLHLVANEYFHDKSLTEIRDSLLDLGDVFPVPLITARYHRDAGAPVYF 439

Db 378 LLMPPFGDILBEEYIGDNGDPQTLQAFQEMWASMFVIRLQVANH--QCSRAPVYF 436
 Qy 440 EFRHRPOCFEDTKPAFYKADHADVRFVFGAFLKGDIVMFEGATEEKLISRKKMKY 499
 Db 437 EFRHRPOCFEDTKPAFYKADHADVRFVFGAFLKGDIVMFEGATEEKLISRKKMKY 499
 Qy 500 TPARTGNPNNDLSLMPAYNLTEOYLQDLNMSLQRLKEPVPVMTSTIP 550
 Db 493 NFRANGPNNGEGLPHWPLFDQEEQYQLNLTQAVRALKAHRLQWKKALP 543

RESULT 3
 US-09-949-016-6426
 / Sequence 6426, Application US/09949016
 / Patent No. 6812339
 / GENERAL INFORMATION:
 / APPLICANT: VENTER, J. Craig et al.
 / TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 / WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 / FILE REFERENCE: CL001307
 / CURRENT APPLICATION NUMBER: US/09/949,016
 / PRIOR FILING DATE: 2000-04-14
 / PRIOR APPLICATION NUMBER: 60/241,755
 / PRIOR FILING DATE: 2000-10-20
 / PRIOR APPLICATION NUMBER: 60/237,768
 / PRIOR FILING DATE: 2000-10-03
 / PRIOR APPLICATION NUMBER: 60/231,498
 / NUMBER OF SEQ ID NOS: 207012
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO: 6426
 / LENGTH: 559
 / TYPE: PRT
 / ORGANISM: Human
 US-09-949-016-6426

Query Match 39.9%; Score 1230; DB 4; Length 559;
 Best Local Similarity 46.7%; Pred. No. 4.8e-125;
 Matches 248; Conservative 91; Mismatches 168; Indels 24; Gaps 8;
 Qy 31 GPSAEGPQNTRLGMIQKQVTVLGSVPVNVFLGVFPAPPLGSLRFTNPQASPMWDL 90
 Db 26 GQDSASPIRTTHGQVLSLVHVKGANAGVQTFGLGIPFAKPLGLRFAPEPPESMGV 85
 Qy 91 REATSYENLCLQN-----SEWLLDQMLKVHPKRGVSEDCLYINITYAPAHADTGSKL 145
 Db 86 RDGTHPACLODLTAVESEFL-----SQPNMTFSPDSMEDCLYISTTPAHSHSGSNLP 141
 Qy 146 VLVWFGGAFKTSASIFDGSALAAVEDLVVVVVOYRGLIGFTFTWQOHPGNWAFDQ 205
 Db 142 VVWVINGGLVVGMSLVDSMLALENVVVYIIYRLGVIGFSTGDKHATGMWGYLDQ 201
 Qy 206 VVALSVQKNIIEFGGDPSSVTIFGESAGATSVSLISLSPAKGLFKAHAIWESGVAII 265
 Db 202 VVALSVQKNIIEFGGDPSSVTIFGESAGATSVSLISLSPAKGLFKAHAIWESGVAII 265
 Qy 266 LEAHYKSEDI--OVVAHFCGNNADEBALRLCLRTSPSKELLTTSOKTSFTRVVDGA 323
 Db 262 LIA-----SSADVISTVAVNLACQDVDEBALVGCIRKSGKEIILAIKPKFMIPGVVDG 317
 Qy 324 FFPNEPDLISOKAFKAPSIIGVNHCGFLP-----MKAPBILSGNSKSLAHLIQL 379
 Db 318 FLPRHPQELASADQAPVPSIVGNNEFGWILPKWRIYDTQKEMREASQAALQKMLT 377
 Qy 380 ILHLPQYLHLVANEYFHDKSLTEIRDSLLDLGDVFPVPLITARYHRDAGAPVYF 439
 Db 378 LLMPPFGDILBEEYIGDNGDPQTLQAFQEMWASMFVIRLQVANH--QCSRAPVYF 436
 Qy 440 EFRHRPOCFEDTKPAFYKADHADVRFVFGAFLKGDIVMFEGATEEKLISRKKMKY 499
 Db 437 EFRHRPOCFEDTKPAFYKADHADVRFVFGAFLKGDIVMFEGATEEKLISRKKMKY 499

QY 500 TPARTGNNGNDLSLMPAYNLTEOYLQDLNLSLQGLKEPRVDFTWSTIP 550
Db 493 NFARNGNNGEGCLPHWPLFDQEBQYLQNLQPAVGRALKAHRLQFWKALP 543

RESULT 4
US-09-949-016-9670
Sequence 9670, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9670
LENGTH: 577
TYPE: PRF
ORGANISM: Human
US-09-949-016-9670

Query Match 39.9%; Score 1230; DB 4; Length 577;
Best Local Similarity 46.7%; Pred. No. 5,1e-125;
Matches 248; Conservative 91; Mismatches 168; Indels 24; Gaps 8;

QY 31 GPSAEGPQNRRLGHIQKQVTVLGSVPVNVFLGVPAPPLGSLRTNPOAPMNDL 90
Db 44 GDSASPIRTHHTGVLGSLVHVKNAGNVOTFLDIIPAKPPLGLRPAPEPPESWGV 103
QY 91 REATSPMLCION-----SEWLLDQHLKHYPKFVSEDCLYNITAPAPADGSKLP 145
Db 104 RDGTHPMACLODLTAVSEBFL-----SQNMFTFSDSSEDCLYSTTPAHSHGSKLP 159
QY 146 VLWPFPGAFKTSASIFDGSALAAVEDVLVVVVOYRLGIFGFTWDOHAPGNNAFKDQ 205
Db 160 VMVWTHGALVFGMASLVDGSLALBNVYVYIIQYRLGVGFSTGDKHAGMNGYLDQ 219
QY 206 VAALSVMQKNIIEFGGDPSSVTTFGESAGALSVSLLISPMAGLPHKALMESGVAIIPY 265
Db 220 VAALEWVOQNIHAFGNDPRVTIFGESAGTSVSSLVVSPISQGLFHGALMESGVALLPG 279
QY 266 LEAHYKESBDL--QVNAHFGCNMNSDSEALLRCRTPKSKELLTLSQKTSFTVVDGA 323
Db 280 LIA-----SSADIVSTVAVNLASCDQVDSBALGCLRGSKKEILLAINPKKPIPGVVDGV 335
QY 324 FFPNEPLDLSQAKFAIPSIIGVNNHCGFLP-----MKEAPEILSGSNKSLALHLION 379
Db 336 FLPRHPOGLLASADQPPPSIVGVNNHNGWMLIPYMIYDTQKMDREASQAALQKMLT 395
QY 360 ILHIPPQYLAHVANVEYFHDKSLTEIRDSLDDLDGVFFVVPALITARYHDAQAPVYFY 439
Db 396 LLMLPPTGDLRLREYIGNDGDPQTLQAOFOQEMADSMFVIRPALQVAF--QCSRAPVYFY 454
QY 440 EPRHAPQCFEDTKRPAFVADHAEVRFVFGAFLGDIIVMPEGATEEELKLSRKMCKWA 499
Db 455 EFQHPSPMLKNIIRPHMKADHGDDELRFVF--RSFEGGNIYKF--TEEBEQSLRKMCKWA 510
QY 500 TPARTGNNGNDLSLMPAYNLTEOYLQDLNLSLQGLKEPRVDFTWSTIP 550
Db 511 NFARNGNNGEGCLPHWPLFDQEBQYLQNLQPAVGRALKAHRLQFWKALP 561

RESULT 5
US-09-595-682B-21

Sequence 21, Application US/09595682B
Patent No. 6800483
GENERAL INFORMATION:

APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 565
TYPE: PRF
ORGANISM: Oryctolagus cuniculus
US-09-595-682B-21

Query Match 37.4%; Score 1150.5; DB 4; Length 565;
Best Local Similarity 43.9%; Pred. No. 2,5e-116;
Matches 252; Conservative 75; Mismatches 180; Indels 67; Gaps 13;

QY 12 WCFPLIQLPLGHQWKGTSAGSPQNRRLGHIQKQVTVLGSVPVNVFLGVPAP 71
Db 2 WLCALALSLACIACIACIACIACIACIACIACIACIACIACIACIACIACIACI 58
QY 72 PLGSLRFTNPOAPSPMDNLREATSPMLCIONSEWLLDQHL-----KHYAP-KGV 123
Db 59 PLGSLRFTNPOAPSPMDNLREATSPMLCIONSEWLLDQHL-----KHYAP-KGV 112
QY 124 SEDCLYNTIYAPADGSKLPVLWPFPGAFKTSASIFDGSALAAVEDVLVVVVOYRL 183
Db 113 SEDCLYNTIYAPADGSKLPVLWPFPGAFKTSASIFDGSALAAVEDVLVVVVOYRL 172
QY 184 GIFGFTWDOHAPGNNAFKQVNAALSVQKNIIEFGGDPSSVTTFGESAGALSVSLL 243
Db 173 GIFGFTWDOHAPGNNAFKQVNAALSVQKNIIEFGGDPSSVTTFGESAGALSVSLL 232
QY 244 SPMAKGLFHKAIMESGVAIIPYLAHDEKSED--LQVNAHFGCNMNSDSEALLRCRTK 301
Db 223 SPLTKNLFHRAISGVALLSL-----FRKNTKSLAEKIALIAGCKTTSVAVMHCRLQK 288
QY 302 PSKELL--TLSQK-----TKSPTRVVDGAFFNEPLDLSQAKFAIPSIIG 346
Db 289 TEBELMEVTLKMKEMALDLVDPKENTAFITTVIDGVLLPAPAPAILAEKYNMLPYMG 348
QY 347 VNNHCEGFLPM-----KEAPEILSGSNKSLALHLIONLHITPROYLHVA 392
Db 349 INOGEFMIIPMOMGLYPLSEGLDQKATLMLKS-----YPLVANSKELTPVAT 399
QY 393 NEYFHDKSLTEIRDSLDDLDGVFFVVPALITARYHDAQAPVYFYEFRRHPOCFEDTK 452
Db 400 EKLIGCTDDPKKCDLFLDMLADLLFGVPSVAVARHHRDAGAPTYMYEYRTRPSSDMR 459
QY 453 PAFVADHAEVRFVFGAFLKGDIVNEEGATEEELKLSRKMCKWATPAPATGNDL 512
Db 460 PKTVIGDHDEIFSLYGLAPFLK-----EGATEEELKLSKVMYKWFANFARNGNNGEGCL 513
QY 513 SLMPAYNLTEOYLQDLNLSLQGLKEPRVDFTWSTIP 550
Db 514 PMPAYDYKESYLOIGATTQAQKDKKEVAFWT 547

RESULT 6
US-09-264-737-2
Sequence 2, Application US/09264737A
Patent No. 6107549
GENERAL INFORMATION:

APPLICANT: Feng, Paul C.C.
APPLICANT: Ruff, Thomas G.
TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
TITLE OF INVENTION: Expression of Esterase Enzymes
FILE REFERENCE: 38-21(10551) PLE3 Pyridine Tolerance
CURRENT APPLICATION NUMBER: US/09/264,737A
CURRENT FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: 60/077,377
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 566
TYPE: PRT
ORGANISM: Rabbit
US-09-264-737-2

Query Match 37.0%; Score 1138.5; DB 3; Length 566;
Best Local Similarity 43.6%; Pred. No. 5.1e-115;
Matches 250; Conservative 75; Mismatches 176; Indels 73; Gaps 14;

QY 12 WCFLLLOPLGHRQMGKTGSPSABGPQRTRLGWIQKQVTVLGSPPVNVFLGVPFAAP 71
DB 9 WLF-----IACTAMGH--PSAP--PVVDYVKGVLGKFSLEGPAGVAVFLGVPFAKP 59
QY 72 PLGSLRFTNPOPASPMNDLREATSYPNLCLNSEMLLDQML-----KVHYP-KFV 123
DB 60 PLGSLRFAFPQPAESMSHVKNKTTSTPWCSDA-----VSGHMLSELFTNRKENIPLKF-- 113
QY 124 SEDCLYINITYAPAHADTSGKLPVLVWFPFGAFKTSASIFDGSALAAVEDLVVVVQYRL 183
DB 114 SEDCLYINITYPADLTGRRLPVVWVWVHGGGLMGAGASTYDGLALSHENVVVTTIOYRL 173
QY 184 GIFGFTTMDHAPGNMAFKQOVAALSWOKNIEFGDPSVTTFESAGAISVSSLIL 243
DB 174 GIMGFSTGDSHSGNMCHLDQVAALKRVQDNINFGDPSVTTFESAGAGSVSTILL 233
QY 244 SPMAKGLFHKAIMESGVAIIPYLEANDYKESD--LQVVAHFCGNNADEBALLRCIRTK 301
DB 234 SPLTKNLFHRAISSEGVALLSSL--FRKNTKSLAKKIALKAGCKTTTSAAVWHCLROK 289
QY 302 PSKELL--TISQK-----TKSFTRVVDGAFPNNEBLDLSQKAFAPISIIIG 346
DB 290 TEEELMEVTLKMKMALDVGDPKENTAFLLTVIDGVLKPAKAEILAEKKVMMLPYMG 349
QY 347 VNNHECGFLPM-----KEAPEILSGNSKSLALHLINILHIIPQYLAHA 392
DB 350 INOGEFGMIIPMQLGYPLSEGLDKQKATLMLKS-----YPIVNSKELTPVAT 400
QY 393 NEYFHDGSLTEIRDSLLDLGVPFVVPALITARYHRDAGAVYFYEFRHRPOCFEDTK 452
DB 401 EKYIGTDDPVKKKDLFLDLMLADLFGVPSVNVARHHRDAGAPTYVEYRYPSPSSDMR 460
QY 453 PAFVKAHDADEVAFVFGAFGLKGDIVMFGATEEELSLSRKMKKYATFARNGNDL 512
DB 461 PKTVIGDHGEIRSVLGAFLK-----EGATEEELKLSKMKWAKYANFARNGNPGGL 514
QY 513 SLWPAYNLTEQYIQLDLNNSLGRLEKPRVDFWT 546
DB 515 POWPAYDYKEGYLIQATTQAQKLDKEVAFWT 548

RESULT 7
US-09-595-682B-26
Sequence 26, Application US/09595682B
Patent No. 6800483
GENERAL INFORMATION:
APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of
FILE REFERENCE: SJ-0005

CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 543
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-595-682B-26

Query Match 36.7%; Score 1130.5; DB 4; Length 543;
Best Local Similarity 43.7%; Pred. No. 3.5e-114;
Matches 249; Conservative 75; Mismatches 179; Indels 67; Gaps 13;

QY 12 WCFLLLOPLGHRQMGKTGSPSABGPQRTRLGWIQKQVTVLGSPPVNVFLGVPFAAP 71
DB 2 WLCALALASLAACAMGH--PSAP--PVVDYVKGVLGKFSLEGPAGVAVFLGVPFAKP 58
QY 72 PLGSLRFTNPOPASPMNDLREATSYPNLCLNSEMLLDQML-----KVHYP-KFV 123
DB 59 PLGSLRFAFPQPAESMSHVKNKTTSTPWCSDA-----VSGHMLSELFTNRKENIPLKF-- 112
QY 124 SEDCLYINITYAPAHADTSGKLPVLVWFPFGAFKTSASIFDGSALAAVEDLVVVVQYRL 183
DB 113 SEDCLYINITYPADLTGRRLPVVWVWVHGGGLMGAGASTYDGLALSHENVVVTTIOYRL 172
QY 184 GIFGFTTMDHAPGNMAFKQOVAALSWOKNIEFGDPSVTTFESAGAISVSSLIL 243
DB 173 GIMGFSTGDSHSGNMCHLDQVAALKRVQDNINFGDPSVTTFESAGAGSVSTILL 232
QY 244 SPMAKGLFHKAIMESGVAIIPYLEANDYKESD--LQVVAHFCGNNADEBALLRCIRTK 301
DB 233 SPLTKNLFHRAISSEGVALLSSL--FRKNTKSLAKKIALKAGCKTTTSAAVWHCLROK 288
QY 302 PSKELL--TISQK-----TKSFTRVVDGAFPNNEBLDLSQKAFAPISIIIG 346
DB 289 TEEELMEVTLKMKMALDVGDPKENTAFLLTVIDGVLKPAKAEILAEKKVMMLPYMG 348
QY 347 VNNHECGFLPM-----KEAPEILSGNSKSLALHLINILHIIPQYLAHA 392
DB 349 INOGEFGMIIPMQLGYPLSEGLDKQKATLMLKS-----YPIVNSKELTPVAT 399
QY 393 NEYFHDGSLTEIRDSLLDLGVPFVVPALITARYHRDAGAVYFYEFRHRPOCFEDTK 452
DB 400 EKYIGTDDPVKKKDLFLDLMLADLFGVPSVNVARHHRDAGAPTYVEYRYPSPSSDMR 459
QY 453 PAFVKAHDADEVAFVFGAFGLKGDIVMFGATEEELSLSRKMKKYATFARNGNDL 512
DB 460 PKTVIGDHGEIRSVLGAFLK-----EGATEEELKLSKMKWAKYANFARNGNPGGL 513
QY 513 SLWPAYNLTEQYIQLDLNNSLGRLEKPRVDFWT 542
DB 514 POWPAYDYKEGYLIQATTQAQKLDKEVAFWT 543

RESULT 8
US-08-845-295A-2
Sequence 2, Application US/08845295A
Patent No. 5817490
GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Process for the Manufacture of
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
STREET: P. O. Box 511
CITY: Kingsport

STATE: Tennessee
COUNTRY: USA
ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,295A
FILING DATE: 25-April-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-08-845-295A-2

Query Match 35.4%; Score 1091.5; DB 2; Length 584;
Best Local Similarity 43.8%; Pred. No. 7.4e-110;
Matches 259; Conservative 63; Mismatches 191; Indels 79; Gaps 17;

QY 12 WCFPLILQPLGHRMGKTPSABGQPNTRLGWIQKQVTV--LGSPVPVNVFLGVPPA 69
DB 2 WLLPVLTLSSASATW--AGOPASPPVVDVTAQGRVLGKTVSLEGLAFTQPVAVFLGVPPA 59
QY 70 APPLGSLRFTNPOPAPSPMDNLEATSYPNLCLONS--EWLLD-----QHMLKVHYPK 120
DB 60 KPPLSGLRFPAPQAPLPPSPVNTTSYPPMCCODPVVEQMSDLEFTNFGKRLTLBF-- 117
QY 121 FGVSDECLYLNLYAPAHADTSGKLPLYLVWFPDGAFTKGSASIFDGSALAAYED--VLVVV 178
DB 118 ---SEDCLYLNLYTPADLTGKGRPLPVWVWIHGGGLVLGAPMYDGVVLAHNFVVVVA 174
QY 179 VOYRIGIGFPGFTTWOAHAGNNAFKDOVAALSWQKNIFFGSGDSSVTIFGES--AGAI 236
DB 175 IQYRIGIGWFGFTGDEHSRGNMGHLDQVAALHWQENIANFGDDPGSVTIFGESFPAAGE 234
QY 237 SVSLSILSPMAKGLPHKAIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDSEALLR 296
DB 235 SVSVLVLSPLAKNLFHRAISESGVALTVALLVRKDMAAKQIAVLACGCTTTSAVFTFVH 294
QY 297 CLRTKPSKELLTISOXTKSF-----RVVDGAFFPNEPDLISOK--AFK 339
DB 295 CLRQSEDELDLTLTKMKFLTLDFHGDQRESHPLFTVVDGVLLPKMPEEILAKDFTFN 354
QY 340 AIPSLIIVNNHSGFLP-----MKEABELISGSKSLALHILIONILHIPPQ 386
DB 355 TVPYIYIGIKQEGGMLPTMGMGFPLESGKLDQKTATSLMKS-----YPIANI-----PE 404
QY 387 YHLVLANEYFHDKX-----SLTEIRPSLLDLDGVFVVPALITAYHNDAGAPVYFYEF 441
DB 405 ELTPVAT--FTDKYLGSTDDPVKKKDLFLDLMGDDVFGVSVVAQHNDAGAPPTMYEF 462
QY 442 RHHPQCFED--TKPAFVKAHDADEVFVFGAFLKGDIVMFEQATEEKKLSRKMKYNA 499
DB 463 QYRPSASSDKFTYKPKYVIGDHDGEIFSVGFLLKDD-----APEEELSLSLTKWKFPA 516
QY 500 TPARTGNPNNGNDLSLWP--AYNLTEOYLQDLNMSIGORLKEBRVDFWTSTI 549
DB 517 NFARSGNPNQEGELPHWPFMTYDQEBGYLDIGVYTAAKRLKGBEVAFFMNDLL 568

RESULT 9
US-09-140-933-2
Sequence 2, Application US/09140933
Patent No. 6022719

GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Process for the Manufacture of
TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of
TITLE OF INVENTION: 2-Keto-L-Gulonic Acid
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
STREET: P. O. Box 511
CITY: Kingsport
STATE: Tennessee

COUNTRY: USA
ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/140,933
FILING DATE: 27-August-98
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
FILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-09-140-933-2

Query Match 35.4%; Score 1091.5; DB 3; Length 584;
Best Local Similarity 43.8%; Pred. No. 7.4e-110;
Matches 259; Conservative 63; Mismatches 191; Indels 79; Gaps 17;

QY 12 WCFPLILQPLGHRMGKTPSABGQPNTRLGWIQKQVTV--LGSPVPVNVFLGVPPA 69
DB 2 WLLPVLTLSSASATW--AGOPASPPVVDVTAQGRVLGKTVSLEGLAFTQPVAVFLGVPPA 59
QY 70 APPLGSLRFTNPOPAPSPMDNLEATSYPNLCLONS--EWLLD-----QHMLKVHYPK 120
DB 60 KPPLSGLRFPAPQAPLPPSPVNTTSYPPMCCODPVVEQMSDLEFTNFGKRLTLBF-- 117
QY 121 FGVSDECLYLNLYAPAHADTSGKLPLYLVWFPDGAFTKGSASIFDGSALAAYED--VLVVV 178
DB 118 ---SEDCLYLNLYTPADLTGKGRPLPVWVWIHGGGLVLGAPMYDGVVLAHNFVVVVA 174
QY 179 VOYRIGIGFPGFTTWOAHAGNNAFKDOVAALSWQKNIFFGSGDSSVTIFGES--AGAI 236
DB 175 IQYRIGIGWFGFTGDEHSRGNMGHLDQVAALHWQENIANFGDDPGSVTIFGESFPAAGE 234
QY 237 SVSLSILSPMAKGLPHKAIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDSEALLR 296
DB 235 SVSVLVLSPLAKNLFHRAISESGVALTVALLVRKDMAAKQIAVLACGCTTTSAVFTFVH 294
QY 297 CLRTKPSKELLTISOXTKSF-----RVVDGAFFPNEPDLISOK--AFK 339
DB 295 CLRQSEDELDLTLTKMKFLTLDFHGDQRESHPLFTVVDGVLLPKMPEEILAKDFTFN 354

[illegible]

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1 RESULT 10
2 US-09-146-661-2
3 / Sequence 2, Application US/09146661
4 / Patent No. 6136575
5 /
6 / GENERAL INFORMATION:
7 / APPLICANT: Hubbs, John C.
8 / TITLE OF INVENTION: Enzymatic Process for the Manufacture of
9 / TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of 2-Keto-L-Gu
10 / TITLE OF INVENTION: Acid
11 / NUMBER OF SEQUENCES: 3
12 / CORRESPONDENCE ADDRESSES:
13 / ADDRESSER: Eastman Chemical Company
14 / STREET: P.O. Box 511
15 / CITY: Kingsport
16 / STATE: Tennessee
17 / COUNTRY: USA
18 / ZIP: 37662-5075
19 / COMPUTER READABLE FORM:
20 / MEDIUM TYPE: 3.5 inch disk
21 / COMPUTER: IBM Compatible
22 / OPERATING SYSTEM: Windows 95
23 / SOFTWARE: Microsoft Word
24 / CURRENT APPLICATION DATA:
25 / APPLICATION NUMBER: US/09/146, 661
26 / FILING DATE: 03-September-98
27 / CLASSIFICATION:
28 / PRIOR APPLICATION DATA:
29 / APPLICATION NUMBER: US 60/017, 879, 08/845,295
30 / FILING DATE: 17-May-96, 25-April-97
31 / ATTORNEY/AGENT INFORMATION:
32 / NAME: Cheryl U. Tubach
33 / REGISTRATION NUMBER: 38,346
34 / REFERENCE/DOCKET NUMBER: 70432
35 / TELECOMMUNICATION INFORMATION:
36 / TELEPHONE: 423-229-1239
37 / TELEFAX: 423-229-6189
38 / INFORMATION FOR SEQ ID NO: 2:
39 / SEQUENCE CHARACTERISTICS:
40 / LENGTH: 584 amino acids
41 / TYPE: Amino Acid
42 / TOPOLOGY: Linear
43 /
44 / MOLECULE TYPE: protein
45 /
46 / US-09-146-661-2

```

Query March	35.4%	Score 1091.5;	DB 3;	Length 584;
Best Local Similarity	43.8%	Pred. No. 7.4e-110;		
Matches 259;	Conservative 163;	Mismatches 191;	Indels 79;	Gaps 177;
QY	12	MCFELLLOPLLGHROMGKTGPEAEGRQKNTLGMIGIOKQTV--LGSPPVAVNFIAGVPPA	69	
Db	2	WLLPLVLTSLASSATM--AGQPAAPSPVVDITQGVNLKIVSLGCLAFTPVAVFIAGVPPA	59	
QY	70	APPLGLSRRTNQQPASPVDNIREATSPFNICLONS--EWLLID-----QHWLKHVHPK	120	
Db	60	KPPLSLRPAAPQAPAPSPVAKNTTSPVPMCCQDPVVEQMTSLFTFNFGKRLTLER--	117	

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QY 121 FGVSDDCLXNITYA PAADTGSCLPLVLPVWPGCAFRTGSSATFDGSAALAYED--VLVVV 178
Db 118 ---SBDCLXNITYPLADLTTRGRGLPVMWVHGGGLVLTGAPAPYDGVLLAAHENTVVVVA 174
QY 179 VOYRLGIFGFFFTTMDQAPGNMAFKDOVALSMVOKNIEFGGDPSSVTFEGES--AGAI 236
Db 175 IQYRLGIMGFESTGDESHSGNMGHLDQVAAALMVOENIANFGCDPGSVTLTFGESFTLGE 234
QY 237 SVSLIISPAKGLPHKALMESVAILPLEAHYDEKEDIQVVAHFQGNNAASDEALLR 296
Db 235 SVSLVLSPLAKULFRAAISGVALVYALVRKKMAAKOIAIACGKTTTSVTFVH 294
QY 297 CLRTPEKELLTLTQTKSFST-----RVDDAFFFNPELLTLTQK--APR 339
Db 295 CLRKQSEDELLDTLTCKKFLTLDPHQDQRESHRPLPVYDGVLLPKPBEILAEKOPTF 354
QY 340 AIRSIIGVNNHEGFLLP-----MKAPETLSGSNKSLALHLIONILHI PRO 386
Db 355 TWPYIVGINKQEGWMLPTMGWFFLSEBGLDOKTATSLMWKS-----YLIANI-----PE 404
QY 387 YLHLVANEYFHDHKG-----SLTEIRDSLLDLGGVFVFPVALLTARVYHDAQPVYFEEF 441
Db 405 ELTPVAT--FTDKXVLGTDGDDPYKKDLFLDLMGVAVGCVSVVAQOHNDAGAPTYMEEF 462
QY 442 RHHPQCFED--TKPAFVYADHADVRFVFGGAFLKGDIVYFEGATEEKLTLSRKMKYWA 499
Db 463 QYRPSVSSKFFKPYTVIGDHGDEIRFVGFGRPLKGD-----APREBVSLSKTYMKFWA 516
QY 500 TPAKTGNPGNDLSLMP--AYNLTEOYLODLDMNSGURLKEPRVDVFWSTI 549
Db 517 NFARSGNPGSELPHMPFTWMDQEGTLQIGVNTQAALKKLKEBEVAFWMDLL 568

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RESULT 11
US-09-150-515-2
; Sequence 2, Application US/09150515
; Patent No. 6271006
; GENERAL INFORMATION:
; APPLICANT: Hubbs, John C.
; TITLE OF INVENTION: Enzymatic Process for the Manufacture of
; TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonate Acid, and Esters of
; TITLE OF INVENTION: 2-Keto-L-Gulonate Acid
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eastman Chemical Company
; STREET: P.O. Box 511
; CITY: Kingsport
; STATE: Tennessee
; COUNTRY: USA
; ZIP: 37662-5075
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/150,515
; FILING DATE: 09-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,879; 08/845,295
; FILING DATE: 17-May-96; 25-April-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Cheryl J. Tubach
; REGISTRATION NUMBER: 38,346
; REFERENCE/DOCKET NUMBER: 70432
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 423-229-6189
; TELEFAX: 423-229-1239
; INFORMATION FOR SEQ. ID NO.: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 584 amino acids

```


REFERENCE/DOCKET NUMBER: broomfield
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterases
US-08-446-100-26

Query Match 30.6%; Score 942.5; DB 3; Length 454;
Best Local Similarity 44.9%; Pred. No. 9.5e-94;
Matches 200; Conservative 64; Mismatches 150; Indels 31; Gaps 6;

QY 125 EDCYLYIYPAHADTSKLPVLVWFGGAFKTSASIFDGSALAAVEDVLVVVQYRLG 184
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DB 61 IMGFSTGDEHSGNMCHLDQVAALRWVDNIAFSGNGSVTIGESAGESVSLVLS 120
QY 245 PMAKGLFHKAIMESGVAIIPYLEANDYEK--SEDIQVVAHFCGNAASSEALLRCILRTKP 302
DB 121 PLKKNLFHRAISBSGVALSVLWKGDVPLAEQALIRH--GCCTTISAMVCLROKT 177
QY 303 SKELLTISOK-----TKSFTRVVDGAFPPNEBLDLSQKAFKAIPSIIGV 347
DB 178 EEBLETTIKIGNSYIMTYRETQRESTLLGTVIDMLLKTPEELQRENRNHTVPYMWGI 237
QY 348 NNHECGFLPMKEAPEILSGS--NKSALHLION---ILHIPPQYLHVANEYHHDGSL 402
DB 238 NKQEGFMLIPMOLMSYPLSEGLDQKTAMSLGSPILPFAIAKLIEPAIEKYLGTDDT 297
QY 403 TEIRDSLDLDGDFVFPVVPALITARYHDAAPVYFIEFRHRPOCFEDTTPAFVKADHAD 462
DB 298 VKKKDLIDLADLVDFGVSVIYVAHNRDAGAPTYMEFOYRPSFSSDMKPKTVIGDHD 357
QY 463 EVRFVFGAFLKGDIVMEGATEEEKLSRKMVMYATPARTGNPNNDLSIMPAVYLT 522
DB 358 ELFSVFAGAPFLK-----EGASEEERILSKVMKFMANFARNGNPNKGLPHPEYNOKE 411
QY 523 QYLODLNMSLGOBLKEPRVDFTS 547
DB 412 GYLOIGANTQAOKLQKDEVAFAFWTN 436

RESULT 14
US-08-446-100-28
Sequence 28, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broomfield
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterases
US-08-446-100-28

Query Match 30.6%; Score 942.5; DB 3; Length 454;
Best Local Similarity 44.9%; Pred. No. 9.5e-94;
Matches 200; Conservative 65; Mismatches 149; Indels 31; Gaps 6;

QY 125 EDCYLYIYPAHADTSKLPVLVWFGGAFKTSASIFDGSALAAVEDVLVVVQYRLG 184
DB 1 EHCYLYIYTPADLTCKNRLPVMVWVHIGGLMGAISTYDGLALAAHENVVVTIQRIG 60
QY 185 IFGFFTTWDOHAPGNMAFKDOVAALSMVOKNIEFGGDDSVTTIGESAGAISVSLTIS 244
DB 61 IMGFSTGDEHSGNMCHLDQVAALRWVDNIAFSGNGSVTIGESAGESVSLVLS 120
QY 245 PMAKGLFHKAIMESGVAIIPYLEANDYEK--SEDIQVVAHFCGNAASSEALLRCILRTKP 302
DB 121 PLKKNLFHRAISBSGVALSVLWKGDVPLAEQALIRH--GCCTTISAMVCLROKT 177
QY 303 SKELLTISOK-----TKSFTRVVDGAFPPNEBLDLSQKAFKAIPSIIGV 347
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QY 348 NNHECGFLPMKEAPEILSGS--NKSALHLION---ILHIPPQYLHVANEYHHDGSL 402
DB 238 NKQEGFMLIPMOLMSYPLSEGLDQKTAMSLGSPILPFAIAKLIEPAIEKYLGTDDT 297
QY 403 TEIRDSLDLDGDFVFPVVPALITARYHDAAPVYFIEFRHRPOCFEDTTPAFVKADHAD 462
DB 298 VKKKDLIDLADLVDFGVSVIYVAHNRDAGAPTYMEFOYRPSFSSDMKPKTVIGDHD 357
QY 463 EVRFVFGAFLKGDIVMEGATEEEKLSRKMVMYATPARTGNPNNDLSIMPAVYLT 522
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QY 523 QYLODLNMSLGOBLKEPRVDFTS 547
DB 412 GYLOIGANTQAOKLQKDEVAFAFWTN 436

RESULT 15
US-08-446-100-30
Sequence 30, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B

APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broomfield
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEO ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterases
US-08-446-100-30

Query Match 30.6%; Score 942.5; DB 3; Length 454;
Best Local Similarity 44.9%; Pred. No. 9,5e-94;
Matches 200; Conservative 64; Mismatches 150; Indels 31; Gaps 6;

QY 125 EDCLNTYAPAHADTGSKPLVWVFGAFKTSIFDGSALAEVDLVVVVQYRLG 184
DB 1 EHCLNTYITPADLTKKRLPYWNIHGGCLMVGAHSTYDGLAAHENVVVTIQRLG 60
QY 185 IFGFPTTDHAPGNMAFQDVVALSWQNIIEFGDPSVTIFGESAGAISSVLS 244
DB 61 IWFSTGDEHSGRWGHLDDVVALRWQDNASFGNPGSVTIFGESAGSESVALVS 120
QY 245 PMAKLPHKAIWESGVALIPLYEAHDYK--SEDLQVVAHFGNNASDSEALLRLCLRTKP 302
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QY 303 SKELLTTSQK-----TKSFTRVVDGAFPNBPLDLLSOKAFKAPISIIIGV 347
DB 178 EEBLETTTKIGNSVLTWYRETQRHSTLIGTIVIDKMLIKTPEELQRENFHTVPMWGI 237
QY 348 NNHECGFLPMKEAPEILSGS--NKSLLALHLIION--ILHIPPVYLHLVANEYFHDKSL 402
DB 238 NKEQFGWILPMQIMVPSYSEGQLDQKTAMSLSGSPIPLFAIKELIPBATEKYLGTDT 297
QY 403 TEIRDSLDLDCVFPVVPALITARYHRDAGAPVTFYEFRRHPQCEBDTKPAFVKADHAD 462
DB 238 VKKKDLIIDLIDVWVGPSVIVARNHRDAGAPTYWYEFQYRPSFSSDMKPKTVIGDHD 357
QY 463 EYRFFVGGAFLEKGLVMEFEGATEEELSRKXMKWATFARQNPNGNDLSLMPAYNLTE 522
DB 358 ELFSVFGAFLEK-----EGASEEELRUSKMKWKFANFARNGNPWGKGLPHMPEYNQKE 411
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Db 412 GYLDIGANTQAQKDKKEVAFWTN 436
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Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2005, 20:45:08 ; Search time 158 Seconds
(without alignments)
1411.975 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 3079
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Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3079	100.0	581	US-10-023-515-2	Sequence 2, Appli
2	3079	100.0	581	US-10-674-636-2	Sequence 2, Appli
3	3079	100.0	581	US-10-757-262-46	Sequence 46, Appli
4	2915	99.7	575	US-10-451-168-91	Sequence 91, Appli
5	2900	99.2	642	US-10-433-256-10	Sequence 10, Appli
6	2607.5	84.7	581	US-10-451-168-92	Sequence 92, Appli
7	2506	84.6	525	US-10-094-749-3375	Sequence 2375, Ap
8	2597.5	84.4	581	US-10-114-270-196	Sequence 196, App
9	2588.5	84.1	618	US-10-381-898-2	Sequence 2, Appli
10	2454	79.7	469	US-10-104-047-2219	Sequence 2219, Ap
11	1985	64.5	542	US-10-233-933A-2	Sequence 2, Appli

12	1985	64.5	542	16	US-10-233-933A-2	Sequence 4, Appli
13	1780	57.8	356	15	US-10-451-168-93	Sequence 93, Appli
14	1230	39.9	549	9	US-09-925-298-689	Sequence 689, Appl
15	1230	39.9	550	14	US-10-102-806-689	Sequence 689, Appl
16	1230	39.9	549	15	US-10-102-806-689	Sequence 5, Appli
17	1230	39.9	559	16	US-10-267-756-5	Sequence 28, Appli
18	1186.5	38.5	554	9	US-10-858-371-28	Sequence 4, Appli
19	1186.5	38.5	554	15	US-09-895-860-4	Sequence 4, Appli
20	1186.5	38.5	554	16	US-10-377-072-4	Sequence 4, Appli
21	1179.5	38.3	571	11	US-09-911-836-23	Sequence 23, Appli
22	1179.5	38.3	571	11	US-09-833-245-1090	Sequence 1090, Ap
23	1179.5	38.3	571	13	US-10-036-342-23	Sequence 23, Appli
24	1179.5	38.3	571	13	US-10-036-041-23	Sequence 23, Appli
25	1179.5	38.3	571	14	US-10-028-072-542	Sequence 542, App
26	1179.5	38.3	571	14	US-10-035-855-23	Sequence 23, Appli
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28	1179.5	38.3	571	14	US-10-121-049-542	Sequence 542, App
29	1179.5	38.3	571	14	US-10-123-804-542	Sequence 542, App
30	1179.5	38.3	571	14	US-10-470-542	Sequence 542, App
31	1179.5	38.3	571	14	US-10-175-746-542	Sequence 542, App
32	1179.5	38.3	571	14	US-10-176-918-542	Sequence 542, App
33	1179.5	38.3	571	14	US-10-176-921-542	Sequence 542, App
34	1179.5	38.3	571	14	US-10-227-884-210	Sequence 23, Appli
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36	1179.5	38.3	571	14	US-10-137-865-542	Sequence 542, App
37	1179.5	38.3	571	14	US-10-140-474-542	Sequence 542, App
38	1179.5	38.3	571	14	US-10-035-719-23	Sequence 23, Appli
39	1179.5	38.3	571	14	US-10-142-431-542	Sequence 542, App
40	1179.5	38.3	571	14	US-10-143-114-542	Sequence 542, App
41	1179.5	38.3	571	14	US-10-230-163-210	Sequence 210, App
42	1179.5	38.3	571	14	US-10-036-160-23	Sequence 23, Appli
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44	1179.5	38.3	571	14	US-10-142-419-542	Sequence 542, App
45	1179.5	38.3	571	14	US-10-218-631-210	Sequence 210, App

ALIGNMENTS

RESULT 1
US-10-023-515-2
; Sequence 2, Application US/10023515
; Publication No. US20020182636a1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A. J.
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYESTERASE
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-515-2

Query Match	100.0%	Score 3079;	DB 13;	Length 581;
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Db 61 NVFLGVPAAPPLSLRFTNPQASPWDNREATSYENLCLQNSEWILLDQHMLKVHYPK 120
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RESULT 2
US-10-674-636-2
; Sequence 2, Application US/10674636
; Publication No. US20040086922A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Siles-Santiago, Inmaculada
; TITLE OF INVENTION: 5310, A NOVEL HUMAN CARBOXYLSTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-12201
; CURRENT APPLICATION NUMBER: US/10/674,636
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/10/023,515
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-674-636-2

Query Match 100.0%; Score 3079; DB 15; Length 581;
Best Local Similarity 100.0%; Pred. No. 1,1e-277;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQGLTSSASQWCFPLIIOPLLGHROWKGTSPASBPQNTLRIGIIOGKOVYVGSPPV 60
Db 1 MEQGLTSSASQWCFPLIIOPLLGHROWKGTSPASBPQNTLRIGIIOGKOVYVGSPPV 60
Qy 61 NVFLGVPAAPPLSLRFTNPQASPWDNREATSYENLCLQNSEWILLDQHMLKVHYPK 120
Db 61 NVFLGVPAAPPLSLRFTNPQASPWDNREATSYENLCLQNSEWILLDQHMLKVHYPK 120

Qy 121 FGVEDCLYINITYAPAHADTGSKL PVLWMPGCAFKTGSASIPDGSALAYEDVLYVWVQ 180
Db 121 FGVEDCLYINITYAPAHADTGSKL PVLWMPGCAFKTGSASIPDGSALAYEDVLYVWVQ 180
Qy 181 YRLGI FGFEFTTMOHAGNNAFKDQVVALSWQKNIEFGGDPSSVTIIFGESAGAI SVSS 240
Db 181 YRLGI FGFEFTTMOHAGNNAFKDQVVALSWQKNIEFGGDPSSVTIIFGESAGAI SVSS 240
Qy 241 LILSPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAHFCCNNASDSALLRCURT 300
Db 241 LILSPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAHFCCNNASDSALLRCURT 300
Qy 301 KPSEKELLTSQKTSFTRVVDGAFPPNEBPLDLSQKAFKAI PSIIIGVNNHECGFLLPKKE 360
Db 301 KPSEKELLTSQKTSFTRVVDGAFPPNEBPLDLSQKAFKAI PSIIIGVNNHECGFLLPKKE 360
Qy 361 APEILSGNSKSLALHILQNI LHPQYHLVANEYFHDHSLTEIRDSLLDLGDVFFV 420
Db 361 APEILSGNSKSLALHILQNI LHPQYHLVANEYFHDHSLTEIRDSLLDLGDVFFV 420
Qy 421 PALITARYRDAGAPVYFEFRRPQCCEDTKPAFVKADHAEVAFVFGAFKGDIVMF 480
Db 421 PALITARYRDAGAPVYFEFRRPQCCEDTKPAFVKADHAEVAFVFGAFKGDIVMF 480
Qy 481 EGATEEEKLSRKMVKYATFARTGNPNDLSLMPAVNLTEOYLQDLNWSLQRLKEP 540
Db 481 EGATEEEKLSRKMVKYATFARTGNPNDLSLMPAVNLTEOYLQDLNWSLQRLKEP 540
Qy 541 RVDFTSTIPLILSADMHSPLSLTFLSLQPFFFCAP 581
Db 541 RVDFTSTIPLILSADMHSPLSLTFLSLQPFFFCAP 581

RESULT 3
US-10-757-262-46
; Sequence 46, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karichevi, Venkateswarlu
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 44329, 44373, 5164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21655, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: ME103-007P1RNMNM
; CURRENT APPLICATION NUMBER: US/10/757,262
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332

; PRIOR FILING DATE: 2003-09-26
 ; NUMBER OF SEQ ID NOS: 136
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 46
 ; LENGTH: 581
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-757-262-46

Query Match 100.0%; Score 3079; DB 16; Length 581;
 Best Local Similarity 100.0%; Pred. No. 1,1e-277;
 Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPQGLTSASQWCFLLIQLPLIGHQWKGTPSAEGPQNRRLGWIQKQVTVLGSPPV	60
Db	1	MPQGLTSASQWCFLLIQLPLIGHQWKGTPSAEGPQNRRLGWIQKQVTVLGSPPV	60
Qy	61	NVFLGVPPAAPPLGSLRFTNPQPSAEMDLREBATSYPNLCLQNSEWMLLDQMLKVHYPK	120
Db	61	NVFLGVPPAAPPLGSLRFTNPQPSAEMDLREBATSYPNLCLQNSEWMLLDQMLKVHYPK	120
Qy	121	FGVSEDCLYLNIYAPAHADTGSKLPVLVWPGAGFKTGSASIFDGSALAAVEDVLVVVQ	180
Db	121	FGVSEDCLYLNIYAPAHADTGSKLPVLVWPGAGFKTGSASIFDGSALAAVEDVLVVVQ	180
Qy	181	YRLGIFGFTTWDHAPGNMAFKDQVAALSWQKNIIEFGGDPSSVTIFGSAAGASIVSS	240
Db	181	YRLGIFGFTTWDHAPGNMAFKDQVAALSWQKNIIEFGGDPSSVTIFGSAAGASIVSS	240
Qy	241	LILSPMAKGLFHAKAIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDEBALRCLRT	300
Db	241	LILSPMAKGLFHAKAIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDEBALRCLRT	300
Qy	301	KPSKELLTSLQKTSFTFVNDGAFPPNEPLDLSQKAFKAIPSIIGVNNHCGFLPMKE	360
Db	301	KPSKELLTSLQKTSFTFVNDGAFPPNEPLDLSQKAFKAIPSIIGVNNHCGFLPMKE	360
Qy	361	APELISGNSKSLALHILQNIILHIIPQYLHLVANEYFHDKSLTEIRDSLDDLGLGVFVV	420
Db	361	APELISGNSKSLALHILQNIILHIIPQYLHLVANEYFHDKSLTEIRDSLDDLGLGVFVV	420
Qy	421	PALITARYHADAGAVYFYEFRHRPQCFEDTKPAFKADHAEVRFVFGAFLKGDYMF	480
Db	421	PALITARYHADAGAVYFYEFRHRPQCFEDTKPAFKADHAEVRFVFGAFLKGDYMF	480
Qy	481	EGATEBEKSLSRKMKYATPARTGNPNNDLSLMPAYNLTEQYQLDLNMSLGRLKEP	540
Db	481	EGATEBEKSLSRKMKYATPARTGNPNNDLSLMPAYNLTEQYQLDLNMSLGRLKEP	540
Qy	541	RVDFTSTITPILISADMLHSPLSLTFSLSLQPFPPFCAP	581
Db	541	RVDFTSTITPILISADMLHSPLSLTFSLSLQPFPPFCAP	581

RESULT 4
 US-10-451-168-91
 ; Sequence 91, Application US/10451168
 ; Publication No. US20040091969A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SMITHKLINE BEECHAM CORPORATION
 ; APPLICANT: SMITHKLINE BEECHAM P.L.C.
 ; APPLICANT: GLAXO GROUP LIMITED
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP50039
 ; CURRENT APPLICATION NUMBER: US/10/451,168
 ; CURRENT FILING DATE: 2003-11-12
 ; PRIOR APPLICATION NUMBER: PCT/US01/49232
 ; PRIOR FILING DATE: 2000-12-17
 ; PRIOR APPLICATION NUMBER: 60/256,710
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,048
 ; PRIOR FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: 60/260,482

; PRIOR FILING DATE: 2001-01-09
 ; PRIOR APPLICATION NUMBER: 60/264,922
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: 60/266,797
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/276,988
 ; PRIOR FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 60/281,535
 ; PRIOR FILING DATE: 2001-04-04
 ; PRIOR APPLICATION NUMBER: 60/289,622
 ; PRIOR FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 91
 ; LENGTH: 575
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-451-168-91

Query Match 94.7%; Score 2915; DB 15; Length 575;
 Best Local Similarity 97.0%; Pred. No. 2,1e-262;
 Matches 553; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

Qy	12	WCFLLIQLPLIGHQWKGTPSAEGPQNRRLGWIQKQVTVLGSPPVNVFLGVPPAP	71
Db	14	WAIWVLAAP-----TKGPSAEGPQNRRLGWIQKQVTVLGSPPVNVFLGVPPAP	65
Qy	72	PLGSLRFTNPQPSAEMDLREBATSYPNLCLQNSEWMLLDQMLKVHYPKFVSEDCLYLN	131
Db	66	PLGSLRFTNPQPSAEMDLREBATSYPNLCLQNSEWMLLDQMLKVHYPKFVSEDCLYLN	125
Qy	132	IYAPAHADTGSKLPVLVWPGAGFKTGSASIFDGSALAAVEDVLVVVQYRLGIFGFTT	191
Db	126	IYAPAHADTGSKLPVLVWPGAGFKTGSASIFDGSALAAVEDVLVVVQYRLGIFGFTT	185
Qy	192	WDQAHAGNMAFKDQVAALSWQKNIIEFGGDPSSVTIFGSAAGASIVSSLILSPMAKGLF	251
Db	186	WDQAHAGNMAFKDQVAALSWQKNIIEFGGDPSSVTIFGSAAGASIVSSLILSPMAKGLF	245
Qy	252	HKAIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDEBALRCLRTKPSKELLTSLQ	311
Db	246	HKAIMESGVAIIPYLEAHDYKESDLOVVAHFCGNNASDEBALRCLRTKPSKELLTSLQ	305
Qy	312	KTKSFTRVVDGAFPPNEPLDLSQKAFKAIPSIIGVNNHCGFLPMKEAPEILISGNSKS	371
Db	306	KTKSFTRVVDGAFPPNEPLDLSQKAFKAIPSIIGVNNHCGFLPMKEAPEILISGNSKS	365
Qy	372	LALHLIQNIILHIIPQYLHLVANEYFHDKSLTEIRDSLDDLGLGVFVVVPPALITARYRD	431
Db	366	LALHLIQNIILHIIPQYLHLVANEYFHDKSLTEIRDSLDDLGLGVFVVVPPALITARYRD	425
Qy	432	AGAPVYFYEFRHRPQCFEDTKPAFKADHAEVRFVFGAFLKGDYMFEGATEBEKSL	491
Db	426	AGAPVYFYEFRHRPQCFEDTKPAFKADHAEVRFVFGAFLKGDYMFEGATEBEKSL	485
Qy	492	RKMKKYATPARTGNPNNDLSLMPAYNLTEQYQLDLNMSLGRLKEPRVDFTSTITP	551
Db	486	RKMKKYATPARTGNPNNDLSLMPAYNLTEQYQLDLNMSLGRLKEPRVDFTSTITP	545
Qy	552	ILISADMLHSPLSLTFSLSLQPFPPFCAP	581
Db	546	ILISADMLHSPLSLTFSLSLQPFPPFCAP	575

RESULT 5
 US-10-433-256-10
 ; Sequence 10, Application US/10433256
 ; Publication No. US20040081980A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique G.
 ; APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R.
 ; APPLICANT: ARVIZU, Chandra S.; RING, HuiJun Z.
 ; APPLICANT: LEE, Ernestine A.; DING, Li

```

; APPLICANT: HAPALIA, April J.A.; TANG, Y. Tom
; APPLICANT: YUE, Henry; TRIBOULEY, Catherine M.
; APPLICANT: LU, Dying Anna M.; LAL, Preeti G.
; APPLICANT: WARREN, Bridget A.; YANG, Junming
; APPLICANT: CHAMLA, Narinder K.; NGUYEN, Daniel B.
; APPLICANT: GANDHI, Ameena R.; LU, Yan
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
; FILE REFERENCE: PI-0113 USN
; CURRENT APPLICATION NUMBER: US/10/433,256
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/47429
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/254,308
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/256,189
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/257,713
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/262,706
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/266,020
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: 6538080CD1
US-10-433-256-10
```

```

Query Match      94.2%; Score 2900; DB 15; Length 642;
Best Local Similarity 99.5%; Pred. No. 6.36-261;
Matches 548; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```

QY      31 GPSAEGPQNRRLGMIQKQVTVLGSPPVNVFLGVFPFAPPLGSGRFTNPOASPMNDL 90
DB      92 GPSAEGPQNRRLGMIQKQVTVLGSPPVNVFLGVFPFAPPLGSGRFTNPOASPMNDL 151
QY      91 REATSYNLCIQNSEWMLLDQHLKVHYPKFGVSEDCLYNIIYAPAHADTGSRLPYLVWF 150
DB      152 REATSYNLCIQNSEWMLLDQHLKVHYPKFGVSEDCLYNIIYAPAHADTGSRLPYLVWF 211
QY      151 PGCAFKTGSASIFDGSALAAVEDLVVVVQYRIGIFGFTTMOHAPGMAFPDQYVALS 210
DB      212 PGCAFKTGSASIFDGSALAAVEDLVVVVQYRIGIFGFTTMOHAPGMAFPDQYVALS 271
QY      211 WQKNIEFFGSDPSVTIFGESAGAISVSLLISPAKGLFHKAIMESGVAIIPYLEAH 270
DB      272 WQKNIEFFGSDPSVTIFGESAGAISVSLLISPAKGLFHKAIMESGVAIIPYLEAH 331
QY      271 YKSESDIQVVAHFCCGNNASDEALRLCLRTKPSKELLTTSQTKSTTRVVDGAFPPNEPL 330
DB      332 YKSESDIQVVAHFCCGNNASDEALRLCLRTKPSKELLTTSQTKSTTRVVDGAFPPNEPL 391
QY      331 DLSQCAFPAIPSIIGVNNHCEGFLPMKEAPEIISGNSKSLALHLIOMIHLIPROYLHL 390
DB      392 DLSQCAFPAIPSIIGVNNHCEGFLPMKEAPEIISGNSKSLALHLIOMIHLIPROYLHL 451
QY      391 VANEYFHDHSLTEIRDSLLDLDGVFFVVPALITARHYRDAGAVYFEFRRHQCEPD 450
DB      452 VANEYFHDHSLTEIRDSLLDLDGVFFVVPALITARHYRDAGAVYFEFRRHQCEPD 511
QY      451 TKPAFAKADHADEVFVFGAFGLKGDIVMEGATEEELSLRKKMKWATARCPNPN 510
DB      512 TKPAFAKADHADEVFVFGAFGLKGDIVMEGATEEELSLRKKMKWATARCPNPN 571
QY      511 DLSLWPAYLITEOYIQLDLNMSLGRQLKPRVDFTSTPIILSASDMLHSPLSLTFLS 570
DB      572 DLSLWPAYLITEOYIQLDLNMSLGRQLKPRVDFTSTPIILSASDMLHSPLSLTFLS 631
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QY      571 LLOPFFFFCAP 581
DB      632 LLOPFFFFCAP 642
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RESULT 6
US-10-451-168-92
; Sequence 92, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-168-92
```

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Query Match      84.7%; Score 2607.5; DB 15; Length 581;
Best Local Similarity 91.4%; Pred. No. 1e-233;
Matches 499; Conservative 7; Mismatches 25; Indels 15; Gaps 3;
```

```

QY      12 WCFLLIQPLIGHROMKKTGPSAEGPQNRRLGMIQKQVTVLGSPPVNVFLGVFPFAP 71
DB      14 WAIWVLAP-----TKGPSAEGPQNRRLGMIQKQVTVLGSPPVNVFLGVFPFAP 65
QY      72 PLGSLRFTNPOASPMNDLREATSYNLCIQNSEWMLLDQHLKVHYPKFGVSEDCLYN 131
DB      66 PLGSLRFTNPOASPMNDLREATSYNLCIQNSEWMLLDQHLKVHYPKFGVSEDCLYN 125
QY      132 IYAPAHADTGSRLPYLVWPPGAFKTGSASIFDGSALAAVEDLVVVVQYRIGIFGFTT 191
DB      126 IYAPAHADTGSRLPYLVWPPGAFKTGSASIFDGSALAAVEDLVVVVQYRIGIFGFTT 185
QY      192 WQAHAPGNNAFKQOYVALSMWQKNIEFFGSDPSVTIFGESAGAISVSLLISPAKGLF 251
DB      186 WQAHAPGNNAFKQOYVALSMWQKNIEFFGSDPSVTIFGESAGAISVSLLISPAKGLF 245
QY      252 HKAIMESGVAIIPYLEAHDIKESBDIQVVAHFCCGNNASDEALRLCLRTKPSKELLTTSQ 311
DB      246 HKAIMESGVAIIPYLEAHDIKESBDIQVVAHFCCGNNASDEALRLCLRTKPSKELLTTSQ 305
QY      312 KTKSFTFRVVDGAFPPNEPLDLSQCAFPAIPSIIGVNNHCEGFLPMKE--APEILSGSN 369
DB      306 KTKSFTFRVVDGAFPPNEPLDLSQCAFPAIPSIIGVNNHCEGFLPMWRILAAVHTATPSN 365
QY      370 KSLAL-----HLIOMIHLIPROYLHLVANEYFHDHSLTEIRDSLLDLDGVFFVVPALI 424
```

Db 366 RDALASTAGHFRHROH1PPOYLH.VANNEYFHDGSLTEIRDSLLDLGDVFFVVPALI 425
Qy 425 TARVHRDAGAPVYFEEFRRHPOCFEDTTPAPYKADHAEVRFVFGAFLKGDIVMEBEAT 484
Db 426 TARVHRDAGAPVYFEEFRRHPOCFEDTTPAPYKADHAEVRFVFGAFLKGDIVMEBEAT 485
Qy 485 EEBKLSHRKMKMYATFARTGNPNNGNDLSLWPAVNLTEQYLQDLNMSLGQRLKEPRVD 544
Db 486 EEBKLSHRKMKMYATFARTGNPNNGNDLSLWPAVNLTEQYLQDLNMSLGQRLKEPRVD 545
Qy 545 WTSTIP 550
Db 546 WWTGYP 551

RESULT 7

US-10-094-749-2375
Sequence 2375, Application US/10094749
Publication No. US20030219741A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOMYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2375
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2375

Query Match 84.6% Score 2606; DB 15; Length 525;

Best Local Similarity 90.9%; Pred. No. 1,2e-233;

Matches 501; Conservative 0; Mismatches 0; Indels 50; Gaps 1;

Qy 31 GPSAAGPQNRRLGWIQGGQVTVLSSPVVNVFLGVPAAPLGSLRFTNPQASPWNL 90
Db 25 GPSAAGPQNRRLGWIQGGQVTVLSSPVVNVFLGVPAAPLGSLRFTNPQASPWNL 84
Qy 91 REATSYPNLCIONSEWLLDDQMLKVHPKGVSSDCLYLNTYAPAHADTGSKLFLVWVF 150
Db 85 REATSYPNLCIONSEWLLDDQMLKVHPKGVSSDCLYLNTYAPAHADTGSKLFLVWVF 144
Qy 151 PGGAKTGSASIFDGSALAAVEDVWVVOYRLGIFGFTTMDQAPGNMAFKDOVAALS 210
Db 145 PGGAKTGSASIFDGSALAAVEDVWVVOYRLGIFGFTTMDQAPGNMAFKDOVAALS 204
Qy 211 WVQKNIEFFGGDPSSVTIFGESAGAISVSSLISPMAGLFFKAIMSGVALIIFYLEAH 270

Db 205 WVQKNIEFFGGDPSSVTIFGESAGAISVSSLISPMAGLFFKAIMSGVALIIFYLEAH 264
Qy 271 YEKSEDLQVNAHFCGNNADESEALLRCIRTKSPKELLTLISQTKSPTRVNDGAFEPNEPL 330
Db 265 YEKSEDLQVNAHFCGNNADESEALLRCIRTKSPKELLTLISQTKSPTRVNDGAFEPNEPL 324
Qy 331 DLSQKAFKALPSIIGVNNHECGFLPMKEAPEILSGSNKSLAHLIONIIHIPPOYLHL 390
Db 325 DLSQKAFKALPSIIGVNNHECGFLPMKEAPEILSGSNKSLAHLIONIIHIPPOYLHL 384
Qy 391 VANEYFHDKSHLTIRPSLLDLGLGDVFFVVPALITARYHRACAPVYFEEFRRHPOCFED 450
Db 385 VANEYFHDKSHLTIRPSLLDLGLGDVFFVVPALITARYHRACAPVYFEEFRRHPOCFED 424
Qy 451 TKPAFVKADHAEVRFVFGAFLKGDIVMEFEGATEEBEKLSSRKMKMYATFARTGNPNGN 510
Db 425 -----BGATEEBEKLSSRKMKMYATFARTGNPNGN 454
Qy 511 DLSLWPAVNLTEQYLQDLNMSLGQRLKEPRVDFTSTIPLISASDMLHSPSSLTFLS 570
Db 455 DLSLWPAVNLTEQYLQDLNMSLGQRLKEPRVDFTSTIPLISASDMLHSPSSLTFLS 514
Qy 571 LLOPPFFFCAP 581
Db 515 LLOPPFFFCAP 525

RESULT 8

US-10-114-270-196

Sequence 196, Application US/10114270
Publication No. US20040030110A1

GENERAL INFORMATION:

APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Rameeh
APPLICANT: Miller, Charles E.
APPLICANT: Malyanekar, Uriel M.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Paturajan, Meera
APPLICANT: Liu, Ziaohong
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Li, Li
APPLICANT: Vernet, Corine
APPLICANT: Zornhagen, Bryan D.
APPLICANT: Gorman, Linda
APPLICANT: Shenoy, Suresh G.
APPLICANT: Pena, Carol E.A.
APPLICANT: Smithson, Glenda
APPLICANT: Burgess, Catherine E.
APPLICANT: Gerlach, Valerie
APPLICANT: Padigaru, Muralidhara
APPLICANT: Shinkets, Richard A.
APPLICANT: Gangolli, Bha A.
APPLICANT: Taupier Jr., Raymond J.
APPLICANT: Caeman, Stacie J.
APPLICANT: Ji, Weizhen
APPLICANT: Anderson, David W.
APPLICANT: Liette, Mario W.
APPLICANT: Raetelli, Luca
APPLICANT: Edinger, Shlomit R.
APPLICANT: Stone, David J.
APPLICANT: McDougall, John R.
APPLICANT: Rothenberg, Mark E.
TITLE OF INVENTION: No. US20040030110A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-322C
CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906

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; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 196
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-270-196

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Query Match      84.4%; Score 2597.5; DB 15; Length 581;
Best Local Similarity 94.3%; Pred. No. 8.8e-233;
Matches 497; Conservative 4; Mismatches 17; Indels 9; Gaps 3;

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QY 31 GPSAEGPQNRTRLGWIGQKQVTVLGSPPVNVFLGVPPAAPPGLSLRTTNQPPASPMWNL 90
DB 27 GPSAEGPQNRTRLGWIGQKQVTVLGSPPVNVFLGVPPAAPPGLSLRTTNQPPASPMWNL 86
QY 91 REATSYPNCLQNSEWLLDDQMLKVHPKFGVSDCLYLNITYAPAHADTSGKLPVLYWF 150
DB 87 REATSYPNCLQNSEWLLDDQMLKVHPKFGVSDCLYLNITYAPAHADTSGKLPVLYWF 146
QY 151 PGAFRTGSASIFDGSALAAVEDLVVVVQVRLGIFGFTTWDQHPGNAFQKQVVALS 210
DB 147 PGAFRTGSASIFDGSALAAVEDLVVVVQVRLGIFGFTTWDQHPGNAFQKQVVALS 206
QY 211 WQXNIIEFGDPSSVTTFGSAAGISVSSLILSPMAKGLFHKAIMSGVAILPYLEAHD 270
DB 207 WQXNIIEFGDPSSVTTFGSAAGISVSSLILSPMAKGLFHKAIMSGVAILPYLEAHD 266
QY 271 YKESDLOVVAHFCGNNSDSEALLRCLRTPKSKELLTTSQKTSFTRVVDGAFPPNEPL 330
DB 267 YKESDLOVVAHFCGNNSDSEALLRCLRTPKSKELLTTSQKTSFTRVVDGAFPPNEPL 326
QY 331 DLSQKAFKAIPSIIGVNNHCGFLPMKE--APEILSGSNKSLAL-----HLIQIILHI 383
DB 327 DLSQKAFKAIPSIIGVNNHCGFLPMKE--APEILSGSNKSLAL-----HI 384
QY 384 PPOYLHVANBYFHDKSLTEIRDSLLDLGDFVFPVVPALITARYHRDAGAPVYFEFRH 443
DB 385 PPOYLHVANBYFHDKSLTEIRDSLLDLGDFVFPVVPALITARYHRDAGAPVYFEFRH 444
QY 444 RPCCFEDTKPAFYKADHADEVRFVFGAFLKGDIVWFEGATEEKLRSKMMKYATPAR 503
DB 445 RPCCFEDTKPAFYKADHADEVRFVFGAFLKGDIVWFEGATEEKLRSKMMKYATPAR 504
QY 504 TGNPNNGDLSIMAYNLTQYLOLDLNMGLGQRLKXPRVDFTWSTIP 550
DB 505 TGNPNNGDLSIMAYNLTQYLOLDLNMGLGQRLKXPRVDFTWSTIP 551

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RESULT 9
US-10-381-898-2
; Sequence 2, Application US/10381898
; Publication No. US20040086867A1
; GENERAL INFORMATION:
; APPLICANT: AZIMZAI, Yalda; BAUGHN, Mariah R.;
; APPLICANT: BOROMSKY, Mark L.; DING, Li;
; APPLICANT: DUGGAN, Brendan; ELIOTT, Vicki S.;
; APPLICANT: GANDHI, Ameena R.; GRIFFIN, Jennifer A.;
; APPLICANT: HAPALIA, April J.A.; ISON, Craig H.;
; APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;

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; APPLICANT: LEB, Ernestine A.; LU, Dying Aina M.;
; APPLICANT: ARVIZU, Chandra S.; POLICKY, Jennifer L.;
; APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
; APPLICANT: SANJANWALA, Madhusudan M.;
; APPLICANT: TANG, Y. Tom; TRIBOULEY, Catherine M.;
; APPLICANT: CHAMLA, Narinder K.; WALSH, Roderick T.;
; APPLICANT: WAREEN, Bridget; XU, Yumeng;
; TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
; FILE REFERENCE: PI-0233 USN
; CURRENT FILING DATE: US/10/381,898
; PRIOR APPLICATION NUMBER: 2003-10-17
; PRIOR FILING DATE: PCT/US01/30662
; PRIOR APPLICATION NUMBER: US 60/236,947
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,947
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238,864
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/242,323
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/247,581
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/249,519
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,834
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/250,567
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7473645CD1
US-10-381-898-2

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Query Match      84.1%; Score 2588.5; DB 15; Length 618;
Best Local Similarity 94.4%; Pred. No. 6.6e-232;
Matches 491; Conservative 1; Mismatches 5; Indels 23; Gaps 1;

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QY 31 GPSAEGPQNRTRLGWIGQKQVTVLGSPPVNVFLGVPPAAPPGLSLRTTNQPPASPMWNL 90
DB 92 GPSAEGPQNRTRLGWIGQKQVTVLGSPPVNVFLGVPPAAPPGLSLRTTNQPPASPMWNL 151
QY 91 REATSYPNCLQNSEWLLDDQMLKVHPKFGVSDCLYLNITYAPAHADTSGKLPVLYWF 150
DB 152 REATSYPNCLQNSEWLLDDQMLKVHPKFGVSDCLYLNITYAPAHADTSGKLPVLYWF 211
QY 151 PGAFRTGSASIFDGSALAAVEDLVVVVQVRLGIFGFTTWDQHPGNAFQKQVVALS 210
DB 152 PGAFRTGSASIFDGSALAAVEDLVVVVQVRLGIFGFTTWDQHPGNAFQKQVVALS 271
QY 211 WQXNIIEFGDPSSVTTFGSAAGISVSSLILSPMAKGLFHKAIMSGVAILPYLEAHD 270
DB 212 WQXNIIEFGDPSSVTTFGSAAGISVSSLILSPMAKGLFHKAIMSGVAILPYLEAHD 331
QY 271 YKESDLOVVAHFCGNNSDSEALLRCLRTPKSKELLTTSQKTSFTRVVDGAFPPNEPL 330
DB 332 YKESDLOVVAHFCGNNSDSEALLRCLRTPKSKELLTTSQKTSFTRVVDGAFPPNEPL 391
QY 331 DLSQKAFKAIPSIIGVNNHCGFLPM-----HIPOYLH 428
DB 392 DLSQKAFKAIPSIIGVNNHCGFLPM-----HIPOYLH 428
QY 391 VANEYFHDKSLTEIRDSLLDLGDFVFPVVPALITARYHRDAGAPVYFEFRHPOCFED 450
DB 429 VANEYFHDKSLTEIRDSLLDLGDFVFPVVPALITARYHRDAGAPVYFEFRHPOCFED 488
QY 451 TKPAFYKADHADEVRFVFGAFLKGDIVWFEGATEEKLRSKMMKYATPAR 510

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Db 468 TRPAVKADHAEVRFVSGAFLKGDIVMEGATEBEKLSRKMKYMTFARTGNPNCN 548
Qy 511 DLSLMPAYNLTEQOYLQDLNMSLQRLKEPRVDFTWSTIP 550
Db 549 DLSLMPAYNLTEQOYLQDLNMSLQRLKEPRVDFTWSTIP 588

RESULT 10
US-10-104-047-2219
; Sequence 2219, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2219
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2219

Query Match 79.7%; Score 2454; DB 15; Length 469;
Best Local Similarity 99.6%; Pred. No. 1.5e-219;
Matches 467; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 113 MLKVHPKGVSEDCYLNIYAPAHADTGSCLPVLVWPGAFKTSASIFDGSALAAYE 172
Db 1 MLKVHPKGVSEDCYLNIYAPAHADTGSCLPVLVWPGAFKTSASIFDGSALAAYE 60
Qy 173 DVLVVVVQYRLGIFGFTTWDQHPGNMAFKQVAAALSVQKNIIEFGDPSGVITIFGS 232
Db 61 DVLVVVVQYRLGIFGFTTWDQHPGNMAFKQVAAALSVQKNIIEFGDPSGVITIFGS 120
Qy 223 AGAIVSSSLILSPMAKGLPHKAIMESGVAILPYLEADHDEKSEDIQVNAHFGGNASDSE 292
Db 121 AGAIVSSSLILSPMAKGLPHKAIMESGVAILPYLEADHDEKSEDIQVNAHFGGNASDSE 180
Qy 293 ALLRCLRTKPSKELLTLISQKTSFTRVVDGAFFPNEPDLDSQKAFKAIPTIIGVNNHSC 352
Db 181 ALLRCLRTKPSKELLTLISQKTSFTRVVDGAFFPNEPDLDSQKAFKAIPTIIGVNNHSC 240
Qy 353 GFLLPKKEAPEILSGSNKSLALHLIQNLILHIPPQYLAHVANEYFHDKSLTEIRSLDL 412
Db 241 GFLLPKKEAPEILSGSNKSLALHLIQNLILHIPPQYLAHVANEYFHDKSLTEIRSLDL 300
Qy 413 LGDVFVVVVALTTAAYHRDAGAPVYFEBRHRPQCEDETRKAFVADHAEVRFVPGAF 472
Db 301 LGDVFVVVVALTTAAYHRDAGAPVYFEBRHRPQCEDETRKAFVADHAEVRFVPGAF 360
Qy 473 LKGDIVMEGATEBEKLSRKMKYMTFARTGNPNCNLSLMPAYNLTEOYLQDLNMS 532
Db 361 LKGDIVMEGATEBEKLSRKMKYMTFARTGNPNCNLSLMPAYNLTEOYLQDLNMS 420
Qy 533 LGQRLKEPRVDFTWSTIPILISASDMLHSPLSLTFSLSLQPFPPFCAP 581
Db 421 LGQRLKEPRVDFTWSTIPILISASDMLHSPLSLTFSLSLQPFPPFCAP 469

RESULT 11
US-10-233-933A-2
; Sequence 2, Application US/10233933A
; Publication No. US20040214171A1
; GENERAL INFORMATION:
; APPLICANT: Yamashita, Tetsuro
; APPLICANT: Miyazaki, Masao
; TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
; FILE REFERENCE: SHIG FP02US006
; FILE REFERENCE: SHIG FP02US006

; CURRENT APPLICATION NUMBER: US/10/233,933A
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: JP2002-057908
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Felis catus
US-10-233-933A-2

Query Match 64.5%; Score 1985; DB 16; Length 542;
Best Local Similarity 71.7%; Pred. No. 1e-175;
Matches 373; Conservative 60; Mismatches 85; Indels 2; Gaps 2;

Qy 31 GPSAEGPQNRNRLGIGQKQVTVLGSPPVNVVFLGVPAPPLGSLRFTNPSPASPMNL 90
Db 22 GPADAPVSTRGLGVNRKQTVTLGTVVNMFLGIPYAAPPLGLRKQKQKAPALPGNDF 81
Qy 91 BEATSYPNLCLQNSEMLLDQHMLKVHPKGVSEDCYLNIYAPAHADTGSCLPVLVWF 150
Db 82 RNATSYPLCLQDQLEMLVSYQVHLKVRYPKLEASDCYLNIYAPAHADNCSNLPVWVF 141
Qy 151 PGAFKTSASIFDGSALAAYEDVLVVVVQYRLGIFGFTTWDQHPGNMAFKQVAAAL 210
Db 142 PGAFKTSASIFDGSALAAYEDVLVVVVQYRLGIFGFTTWDQHPGNMAFKQVAAAL 201
Qy 211 WVQKNIIEFGDPSGVITIFGSAGAISSVSLILSPMAKGLPHKAIMESGVAILPYL-BAH 269
Db 202 WVQKNIIEFGDPSGVITIFGSAGAISSVSLILSPMAKGLPHKAIMESGVAILPYL-BAH 261
Qy 270 DYKESDEDQVNAHFGGNASDSEALLRCLRTKPSKELLTLISQKTSFTRVVDGAFFPNEP 329
Db 262 GDERKQDQVLAIRICGCHASDSALLOCLRAKPSSELMIDISKULFSPVIDDFPDEP 321
Qy 330 LDLSQKAFKAIPTIIGVNNHSCGFLPMEKAPPEILSGSNKSLALHLIQNLILHIPPQYLAH 389
Db 322 VALLTQKAFNSVPSIIGVNNHSCAPFL-STEFSSEILGSSNSLALYLVTFTFNIPTQYLAH 380
Qy 390 LVANEYFHDKSLTEIRSLDLGQDVFFVVPALTTAAYHRDAGAPVYFEBRHRPQCE 449
Db 381 LVADHYFYNKSPVETIRSDFLDLGQDVFFVVPALTTAAYHRDAGAPVYFEBRHRPQCE 440
Qy 450 DTKPAFVADHAEVRFVPGAFKGDIVMEGATEBEKLSRKMKYMTFARTGNPNCN 509
Db 441 DTKPAFVADHAEVRFVPGAFKGDIVMEGATEBEKLSRKMKYMTFARTGNPNCN 500
Qy 510 NDLSLMPAYNLTEOYLQDLNMSLQRLKEPRVDFTWSTI 549
Db 501 EGVPLMPAYNLTEOYLQDLNMSLQRLKEPRVDFTWSTI 540

RESULT 12
US-10-233-933A-4
; Sequence 4, Application US/10233933A
; Publication No. US20040214171A1
; GENERAL INFORMATION:
; APPLICANT: Yamashita, Tetsuro
; APPLICANT: Miyazaki, Masao
; TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
; FILE REFERENCE: SHIG FP02US006
; CURRENT APPLICATION NUMBER: US/10/233,933A
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: JP2002-057908
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Felis catus
US-10-233-933A-4

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/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 93
/ LENGTH: 356
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-451-168-93

Query Match      57.8%; Score 1780; DB 15; Length 356;
Best Local Similarity 100.0%; Pred. No. 7.1e-157;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      242  IISPAKGLFHAKMESGVALIPYLAADYKESDIQVAHFPGNNAASDEALLRCLRTK 30
      |||
      |||
      |||
DB      17  IISPAKGLFHAKMESGVALIPYLAADYKESDIQVAHFPGNNAASDEALLRCLRTK 76
      |||
      |||
      |||
QY      302  PEKELLTSQTKSFTRVVDGAFPPNPELDLSQKAFKAIPSIIGVNHECGFLLPMKEA 36
      |||
      |||
      |||
DB      77  PEKELLTSQTKSFTRVVDGAFPPNPELDLSQKAFKAIPSIIGVNHECGFLLPMKEA 13
      |||
      |||
      |||
QY      362  PEILSGNKSIALHLIQLNIHLIPQYHLVANEYFHDKSLTEIRDSLLDLIDGVFVVP 42
      |||
      |||
      |||
DB      137  PEILSGNKSIALHLIQLNIHLIPQYHLVANEYFHDKSLTEIRDSLLDLIDGVFVVP 190
      |||
      |||
      |||
QY      422  ALIARVHRDAGAVFYEFERRRPOCEDTKPAFVADHADVRFVFGAFKGDIVNFE 48
      |||
      |||
      |||
DB      197  ALIARVHRDAGAVFYEFERRRPOCEDTKPAFVADHADVRFVFGAFKGDIVNFE 25
      |||
      |||
      |||
QY      482  GATEBEKLSRKMKWATPARGNNGNDLSIMPRYNITEYLOLDLMSLGRLEKPR 54
      |||
      |||
      |||
DB      257  GATEBEKLSRKMKWATPARGNNGNDLSIMPRYNITEYLOLDLMSLGRLEKPR 316
      |||
      |||
      |||
QY      542  VDFWSTIPLILSASDMLHSPLSLTFLSLQPFPPFCAP 581
      |||
      |||
      |||
DB      317  VDFWSTIPLILSASDMLHSPLSLTFLSLQPFPPFCAP 356
      |||
      |||
      |||

RESULT 14
US-09-925-298-689
/ Sequence 689, Application US/09925298
/ Publication No. US20020039764A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA103
/ CURRENT APPLICATION NUMBER: US/09/925,298
/ CURRENT FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05881
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ PRIOR FILING DATE: 1999-03-12
/ NUMBER OF SEQ ID NOS: 846
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 689
/ LENGTH: 549
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (1)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ NAME/KEY: SITE
/ LOCATION: (7)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-298-689

Query Match      39.9%; Score 1230; DB 9; Length 549;
Best Local Similarity 46.7%; Pred. No. 2.6e-105;
Matches 248; Conservative 91; Mismatches 168; Indels 24; Gaps 8

QY      31  GPSASPGPNTLGIQGYVTVGSPVNVVFLVGFEAPAPRIGSLRFTNPQASPMWLU 90
      |||
      |||
      |||
DB      16  GQDSAPRITHTGGVGLSVHVGANAAGVOTFLGIPFAAPRPGPRFAPRPPSPSGV 75
      |||
      |||
      |||

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QY 91 REATSYPNLCLON-----SEWLLDQHLKXHYPKFVSEDCLYNTYAPAHADTGSKL 145
DB 76 RDGTHPAMCLODLYAVESEFL-----SOFNMTFSPDSMSEDCLYSTYTPAHSHSGSNLP 131
QY 146 VLWVFGGAFKTSASIFPGSALAAVEDVLYVVVQYRIGIFGFTTMDQAHGMAAFDQ 205
DB 132 VWWVHGGALVFGMASLYDGSMLAENVVVVIQYRGLGVGFSTGDGKHATGMNGYLDQ 191
QY 206 VAALSWQKNIEFGGDPSSVTTFGESAGALSVSSLLISPMAGLFFHKAIMESGVAIIIPY 265
DB 192 VAALRWQONIAHFGGNPDRTYTFGESAGTSVSVSLVSPISQGLFHGAIMESGVALLPG 251
QY 266 LEADHYKSEDL--QVVAHFGGNASDSEALLRCRTPKSKELLTSGKTSFTYVNDGA 323
DB 252 LIA-----SSADVISTVVAHLSACDQVDSSEALVGLRGKSKKEILAINKPFKMI PGVVDGV 307
QY 324 FFPNEPDLISOKAKPAISIIIGVNNHCGFLP-----MKEAPETLSGSKSLALHLION 379
DB 308 FLPRHPQELASADQVPVPSIVGVNNHFGWLPKVMRIYDTQKEMDEASQALQKMLT 367
QY 360 ILHIPPOYLHVANEYFHDKHSLTEIRDSLDDLGDVFFVVPALITARYHRDAGAPVYFY 439
DB 368 LLMLEPTFGDLREBYIGDNGDPQTLQAQFQEMMADSMFVIALQVAHF--QCSRAPVYFY 426
QY 440 EFRHRPQCFEDTKPAFVYKADHAEVRFYFGAFLLKGDIVMEFGATEEEXLSRKMKTWA 499
DB 427 EFOHQPMSWLKNIRPHMKADHGDDEL.PFVF--RSFPGGNVYIKF--TEEBEQLSRKMKTWA 482
QY 500 TPARNGNNDLSLMPAYNLTEOYLQDLNMSLQRLKEPRVDFTWSTIP 550
DB 483 NFARNGNNGEGLPHMPL.FDQEBQYLQNLQPAVGRALKAHRLQPKWALP 533

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RESULT 15

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US-10-102-806-689
; Sequence 689, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL03P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 689
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-689

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Query Match 39.9%; Score 1230; DB 14; Length 549;
Best Local Similarity 46.7%; Pred. No. 2,6e-105;
Matches 248; Conservative 91; Mismatches 168; Indels 24; Gaps 8;

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QY 31 GPSABGPNLTGLWIGQKQVTVLGSFVVPVNFIVGFAPAPLIGSFTNPPQASPMNDL 90
DB 16 GDDSDSPITRTHTTGOVLGSLVHKGNAGVQFTLGI.PFAKPPGLRFAAPPEPPESWGSV 75
QY 91 REATSYPNLCLON-----SEWLLDQHLKXHYPKFVSEDCLYNTYAPAHADTGSKL 145

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DB 76 RDGTHPAMCLODLYAVESEFL-----SOFNMTFSPDSMSEDCLYSTYTPAHSHSGSNLP 131
QY 146 VLWVFGGAFKTSASIFPGSALAAVEDVLYVVVQYRIGIFGFTTMDQAHGMAAFDQ 205
DB 132 VWWVHGGALVFGMASLYDGSMLAENVVVVIQYRGLGVGFSTGDGKHATGMNGYLDQ 191
QY 206 VAALSWQKNIEFGGDPSSVTTFGESAGALSVSSLLISPMAGLFFHKAIMESGVAIIIPY 265
DB 192 VAALRWQONIAHFGGNPDRTYTFGESAGTSVSVSLVSPISQGLFHGAIMESGVALLPG 251
QY 266 LEADHYKSEDL--QVVAHFGGNASDSEALLRCRTPKSKELLTSGKTSFTYVNDGA 323
DB 252 LIA-----SSADVISTVVAHLSACDQVDSSEALVGLRGKSKKEILAINKPFKMI PGVVDGV 307
QY 324 FFPNEPDLISOKAKPAISIIIGVNNHCGFLP-----MKEAPETLSGSKSLALHLION 379
DB 308 FLPRHPQELASADQVPVPSIVGVNNHFGWLPKVMRIYDTQKEMDEASQALQKMLT 367
QY 360 ILHIPPOYLHVANEYFHDKHSLTEIRDSLDDLGDVFFVVPALITARYHRDAGAPVYFY 439
DB 368 LLMLEPTFGDLREBYIGDNGDPQTLQAQFQEMMADSMFVIALQVAHF--QCSRAPVYFY 426
QY 440 EFRHRPQCFEDTKPAFVYKADHAEVRFYFGAFLLKGDIVMEFGATEEEXLSRKMKTWA 499
DB 427 EFOHQPMSWLKNIRPHMKADHGDDEL.PFVF--RSFPGGNVYIKF--TEEBEQLSRKMKTWA 482
QY 500 TPARNGNNDLSLMPAYNLTEOYLQDLNMSLQRLKEPRVDFTWSTIP 550
DB 483 NFARNGNNGEGLPHMPL.FDQEBQYLQNLQPAVGRALKAHRLQPKWALP 533

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Search completed: June 16, 2005, 20:58:35
Job time : 163 secs

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OM protein - protein search, using 9w model

Run on: June 16, 2005, 20:45:53 ; Search time 168 seconds
(without alignments)
1337.546 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 581
Sequence: 1 MPQGLTSSASQWCFFLLIQP.....PLSLTFLSLIQPFPCAP 581

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size: 30 *or more*

Total number of hits satisfying chosen parameters: 29

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	581	100.0	581	5	ABB79537 Human car
2	581	100.0	581	8	ADQ89094 Human uro
3	551	94.8	575	5	ABP61004 Novel hum
4	400	68.8	525	6	ADA54807 Human pro
5	391	67.3	642	8	ABM84114 Human dia
6	381	65.6	642	5	AAE25025 Human dru
7	340	58.5	356	5	ABP61006 Novel hum
8	329	56.6	469	7	ADB64065 Human pro
9	328	56.5	581	5	ABP61005 Novel hum
10	328	56.5	581	6	ABU54639 Human NOV
11	328	56.5	618	5	ADRI9663 Human dru
12	195	33.6	224	7	ADCC5524 Human car
13	124	21.3	266	5	ABP69056 Human pol
14	55	9.5	124	4	AAO05817 Human pol
15	54	9.3	306	5	AAE20909 Human car
16	51	8.8	84	5	ABG66757 Human nov
17	49	8.4	49	4	AAAI6665 Peptide #
18	49	8.4	49	4	ABB35649 Peptide #
19	49	8.4	49	4	AAAM29149 Peptide #
20	49	8.4	49	4	ABB30482 Peptide #
21	49	8.4	49	4	ABB21078 Protein #
22	49	8.4	49	4	AAAB68842 Human bon
23	49	8.4	49	4	AAAM56465 Human bra
24	49	8.4	49	4	ABG50502 Human liv
25	49	8.4	49	4	AAAM04381 Peptide #

26	49	8.4	49	5	ABG38423 Human pep
27	35	6.0	41	5	AAE20912 Carboxyle
28	31	5.3	542	8	ADF50145 Cat cauxi
29	31	5.3	542	8	ADF50147 Cat cauxi

ALIGNMENTS

RESULT 1
ID ABB79537 standard; protein: 581 AA.
AC ABB79537;
XX 23-SEP-2002 (first entry)
DT
XX Human carboxylesterase family member 53010.
DB
XX Carboxylesterase; enzyme; human; analgesic; neurotropic; antiinflammatory;
KW diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..26
FT /label= Signal_peptide
FT Protein 27..581
FT /label= Mature_protein
FT Domain 44..545
FT /note= "carboxylesterase domain"
FT Region 125..135
FT /note= "predicted carboxylesterase type-B signature"
FT Active-site 219..234
FT /note= "predicted carboxylesterase type-B serine active site"
XX
XX WC200250256-A2.
XX
XX 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-US049075.
XX
XX 18-DEC-2000; 2000US-0256369P.
XX 28-MAR-2001; 2001US-0279508P.
XX
XX (MILL-) MILLENNium PHARM INC.
XX
XX Curtis RMJ, SIlas-Santiago I;
PI WPI; 2002-547936/58.
XX N-PSDB; ABM84302.
XX
XX 53010 nucleic acids, useful for diagnosing and treating e.g. vascular diseases, autoimmune diseases, or neurodegenerative diseases, as surrogate markers, in tissue typing and chromosome mapping.
XX
XX Claim 5; Page 110-111; 122pp; English.
XX
XX The present sequence is the protein sequence of human 53010, a novel protein containing the structural characteristics of a carboxylesterase family member. The invention provides 53010 nucleic acids, antisense molecules, expression vectors, host cells, transgenic animals, 53010 proteins, fusion proteins, antigenic peptides, anti-53010 antibodies and methods for detecting the presence of 53010 polypeptides or nucleic acids, of identifying a compound that binds to the 53010 polypeptides, and of modulating the activity of the polypeptide. The 53010 polypeptides and nucleic acids can act as novel diagnostic and therapeutic agents for controlling disorders involving aberrant or deficient hydrolysis of carboxylic esters. As 53010 mRNA is highly expressed in the central and peripheral nervous system, and its expression is regulated in some rodent pain models, 53010 molecules can also act as novel diagnostic targets and therapeutic agents for controlling neurological disorders, such as pain-

CC related disorders. A claimed method of treating or preventing a disorder
CC (especially a pain-related disorder) characterised by aberrant activity
CC of a 53010-expressing cell involves administering a compound that
CC modulates 53010 activity or expression
XX

Sequence 581 AA;

Query Match 100.0%; Score 581; DB 5; Length 581;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MPOGLTSSASQWCFLLIQPLGHRQWKTGSPSAGPQNTLGMIOGKQVTVLGSPPV 60
DB 1 MPOGLTSSASQWCFLLIQPLGHRQWKTGSPSAGPQNTLGMIOGKQVTVLGSPPV 60
QY 61 NVFLGVFAAPPLGSLRFTNPQASPMWDLREATSYPNLCLQNSWLLDDQHLKHYRK 120
DB 61 NVFLGVFAAPPLGSLRFTNPQASPMWDLREATSYPNLCLQNSWLLDDQHLKHYRK 120
QY 121 FGVSSEDCLYNTIYAPAHADTGSKLPLYVWPPGAFKTSASIFDGSALAAYEDVLVVVQ 180
DB 121 FGVSSEDCLYNTIYAPAHADTGSKLPLYVWPPGAFKTSASIFDGSALAAYEDVLVVVQ 180
QY 181 YRLGIFGEFTTMDQAHAPGNMAFKDOVAALSWQXIEFFGDPSSVTTFGSAGAISSVS 240
DB 181 YRLGIFGEFTTMDQAHAPGNMAFKDOVAALSWQXIEFFGDPSSVTTFGSAGAISSVS 240
QY 241 LILSPMAKGLFHKAIMESGVAIIPYLEAHDYKSEDLQVVAHFCGNNAOSEALLRCLRT 300
DB 241 LILSPMAKGLFHKAIMESGVAIIPYLEAHDYKSEDLQVVAHFCGNNAOSEALLRCLRT 300
QY 301 KPSKELLTLOSQKTSFTRVVDGAFPPNEPLDLSQKAFKAIPIIIGVNNHECGFLPMKE 360
DB 301 KPSKELLTLOSQKTSFTRVVDGAFPPNEPLDLSQKAFKAIPIIIGVNNHECGFLPMKE 360
QY 361 APEILSGNKSALHLIQNLHIPPQYHLVANEYFHDKSLTIRSLDLDGDFEVV 420
DB 361 APEILSGNKSALHLIQNLHIPPQYHLVANEYFHDKSLTIRSLDLDGDFEVV 420
QY 421 PALITARHRAAGAPVYFYEFRHAPQCEPDTKPAFVADNADEVRFVFGAFLKGDIVM 480
DB 421 PALITARHRAAGAPVYFYEFRHAPQCEPDTKPAFVADNADEVRFVFGAFLKGDIVM 480
QY 481 EGATEEBEKLTSRKMMKWTATFARTGNPNDLSIMPAVNLTEOYLQDLNMSLQRLKEP 540
DB 481 EGATEEBEKLTSRKMMKWTATFARTGNPNDLSIMPAVNLTEOYLQDLNMSLQRLKEP 540
QY 541 RVDFWISTITPILISASDMLHSPSLTFLSLQPFFFCAP 581
DB 541 RVDFWISTITPILISASDMLHSPSLTFLSLQPFFFCAP 581
```

RESULT 2

ADQ89094 standard; protein; 581 AA.

ADQ89094;

21-OCT-2004 (first entry)

Human urological disorder related protein 53010 SEQ:46.

urolgical disorder; uropathic; cytostatic; urinary incontinence;
benign prostatic hyperplasia; human.

Homo sapiens.

MO2004065576-A2.

05-AUG-2004.

14-JAN-2004; 2004WO-US000750.

```
PR 15-JAN-2003; 2003US-0440318P.
PR 04-FEB-2003; 2003US-0444783P.
PR 27-MAR-2003; 2003US-0457901P.
PR 08-MAY-2003; 2003US-0468775P.
PR 19-MAY-2003; 2003US-0471614P.
PR 16-JUN-2003; 2003US-0478742P.
PR 18-JUL-2003; 2003US-0488529P.
PR 30-JUL-2003; 2003US-0491156P.
PR 02-SEP-2003; 2003US-0495954P.
PR 26-SEP-2003; 2003US-0506332P.
```

(MILL-) MILLENNIUM PHARM INC.

Karichet V, Silos-Santiago I, Eliasof SD;

WPI, 2004-562167/54.

N-PSDB; ADQ89093.

PT Use of polypeptides related to urological disorders, e.g. 44390, 54181,
PT 211 or for identifying a compound capable of treating a urological
PT disorder or identifying and treating a subject having a urological
PT disorder.

PS Claim 1; SEQ ID NO 46; 542pp; English.

XX The present invention describes the use of polypeptides related to
XX urological disorders for identifying a compound capable of treating a
XX urological disorder, identifying a subject having a urological disorder,
XX or treating a subject having a urological disorder. Also described: (1) a
XX method for identifying a compound capable of treating a urological
XX disorder; (2) a method for identifying a subject having a urological
XX disorder; and (3) a method for treating a subject having a urological
XX disorder. The compound has uropathic and cytostatic activities. The
XX compound is related to urological disorders are useful for identifying a
XX compound capable of treating a urological disorder, identifying a subject
XX having a urological disorder, or treating a subject having a urological
XX disorder. Disorders include urinary incontinence and benign prostatic
XX hyperplasia. The present sequence represents a human urological disorder
XX related protein, which is used in the exemplification of the present
XX invention.

Sequence 581 AA;

Query Match 100.0%; Score 581; DB 8; Length 581;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MPOGLTSSASQWCFLLIQPLGHRQWKTGSPSAGPQNTLGMIOGKQVTVLGSPPV 60
DB 1 MPOGLTSSASQWCFLLIQPLGHRQWKTGSPSAGPQNTLGMIOGKQVTVLGSPPV 60
QY 61 NVFLGVFAAPPLGSLRFTNPQASPMWDLREATSYPNLCLQNSWLLDDQHLKHYRK 120
DB 61 NVFLGVFAAPPLGSLRFTNPQASPMWDLREATSYPNLCLQNSWLLDDQHLKHYRK 120
QY 121 FGVSSEDCLYNTIYAPAHADTGSKLPLYVWPPGAFKTSASIFDGSALAAYEDVLVVVQ 180
DB 121 FGVSSEDCLYNTIYAPAHADTGSKLPLYVWPPGAFKTSASIFDGSALAAYEDVLVVVQ 180
QY 181 YRLGIFGEFTTMDQAHAPGNMAFKDOVAALSWQXIEFFGDPSSVTTFGSAGAISSVS 240
DB 181 YRLGIFGEFTTMDQAHAPGNMAFKDOVAALSWQXIEFFGDPSSVTTFGSAGAISSVS 240
QY 241 LILSPMAKGLFHKAIMESGVAIIPYLEAHDYKSEDLQVVAHFCGNNAOSEALLRCLRT 300
DB 241 LILSPMAKGLFHKAIMESGVAIIPYLEAHDYKSEDLQVVAHFCGNNAOSEALLRCLRT 300
QY 301 KPSKELLTLOSQKTSFTRVVDGAFPPNEPLDLSQKAFKAIPIIIGVNNHECGFLPMKE 360
DB 301 KPSKELLTLOSQKTSFTRVVDGAFPPNEPLDLSQKAFKAIPIIIGVNNHECGFLPMKE 360
QY 361 APEILSGNKSALHLIQNLHIPPQYHLVANEYFHDKSLTIRSLDLDGDFEVV 420
DB 361 APEILSGNKSALHLIQNLHIPPQYHLVANEYFHDKSLTIRSLDLDGDFEVV 420
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DB 361 APELISGNNKSLAHLNLIHIPOYLHLYANEFYHDKSLTELRDLDLGDVFFV 420
QY 421 PALITARYHRDAGAVYEFYEFRRPOCEDTKEPAFVKADHDEVFVFGAFLKGDIMWF 480
DB 421 PALITARYHRDAGAVYEFYEFRRPOCEDTKEPAFVKADHDEVFVFGAFLKGDIMWF 480
QY 481 EGATEEEKLSRKKMKYATWATPARTGNPGNDISLWPAYNLTEQYQLDLNLSLQRLKEP 540
DB 481 EGATEEEKLSRKKMKYATWATPARTGNPGNDISLWPAYNLTEQYQLDLNLSLQRLKEP 540
QY 541 RVDFWTSTIPILSLSDMLHSPSLSTPLSLQPFPPFCAP 581
DB 541 RVDFWTSTIPILSLSDMLHSPSLSTPLSLQPFPPFCAP 581
RESULT 3
ABP61004
ID ABP61004 standard; protein; 575 AA.
AC ABP61004;
XX
XX 10-SEP-2002 (first entry)
DE Novel human protein. SEQ ID 91.
XX
XX Human; cytosolic; vulnary; antiarteriosclerotic; antiparkinsonian;
XX nootropic; neuroprotective; immunosuppressive; haemostatic;
XX antiinflammatory; cardiant; antilicer; virucide; antithyroid;
XX cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
XX wound healing disorders; atherosclerosis; Parkinson's disease;
XX Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
XX inflammation; neoplastic disease; nervous system disorder;
XX cardiovascular disorder; pancreatitis; respiratory disorder;
XX hyperproliferation; systemic autoimmune disease; hyper-immunity;
XX developmental abnormality; gastrointestinal ulceration; neuropathy;
XX haematological disease; metabolic disease; sperm dysfunction;
XX thyroid disorder; hypothyroidism; brain damage; colitis;
XX cone photo-transduction deficiency; neurological disease; stroke;
XX angiogenesis; ovulation deficiency; spinal cord; thyroid gland; heart;
XX trachea; thymus; lymph node; muscular system; obesity; anorexia;
XX growth abnormality; precocious puberty.
XX
XX Homo sapiens.
XX
XX WO200250105-A1.
XX
XX 27-JUN-2002.
XX
XX 17-DEC-2001; 2001WO-US049232.
XX
XX 19-DEC-2000; 2000US-0256710P.
XX 20-DEC-2000; 2000US-0257048P.
XX 09-JAN-2001; 2001US-0260482P.
XX 30-JAN-2001; 2001US-0264922P.
XX 06-FEB-2001; 2001US-0266797P.
XX 19-MAR-2001; 2001US-0276988P.
XX 04-APR-2001; 2001US-0281535P.
XX 08-MAY-2001; 2001US-0289622P.
XX
XX (SMK) SMITHKLINE BEECHAM CORP.
XX (SMK) SMITHKLINE BEECHAM PLC.
XX (GLAX) GLAXO GROUP LTD.
XX
XX Agarwal P, Birkeland M, Cogswell JP, Kadnick KF, Lai Y;
XX Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;
XX WPI; 2002-508784/54.
XX N-PSDB; ABQ86169.
XX
XX Secreted proteins and polynucleotides useful as vaccines for preventing
XX or treating various diseases e.g. cancer, wounds, atherosclerosis,
XX Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
XX

PS Claim 1(a); Page 312-313; 335pp; English.
XX
XX The invention relates to an isolated polypeptide with signal sequences
CC which allow it to be secreted extracellularly or membrane associated. The
CC activity of polypeptides of the invention may be described as,
CC cyrostatic, vulnary, antiarteriosclerotic, antiparkinsonian, nootropic,
CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
CC cardiant, antilicer, virucide, antithyroid, cerebroprotective, anorectic,
CC and metabolic. Polypeptides and polynucleotides of the invention are
CC useful in the treatment, or as a vaccine in the prevention of, cancer,
CC wound healing disorders, infection, atherosclerosis, Parkinson's disease
CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
CC inflammation, neoplastic diseases, nervous system related disorders and
CC cardiovascular disorders, pancreatitis, respiratory disorder,
CC hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC developmental abnormality, gastrointestinal ulceration, neuropathy,
CC haematological diseases, metabolic diseases, sperm dysfunction, thyroid
CC disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC transduction deficiency, neurological diseases, stroke, angiogenesis,
CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC growth abnormalities, and alleviation of precocious puberty. The
CC sequences given in records ABP60965-ABP61019 represent novel human
CC proteins of the invention
XX
XX Sequence 575 AA:
SQ
XX
XX Query Match 94.8%; Score 551; DB 5; Length 575;
XX Best local similarity 100.0%; Pred. No. 0;
XX Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 GPSABGPORNTRLGMIOGQYTVLGSPPVNVFLGVPAPPLGSLRFTNPQASPMDNL 90
DB 25 GPSABGPORNTRLGMIOGQYTVLGSPPVNVFLGVPAPPLGSLRFTNPQASPMDNL 84
QY 91 REATSYPLCLQNSBWLDDHMKVHKPKGVSEDCYINITYAPAHADTSSKLPVLMWF 150
DB 85 REATSYPLCLQNSBWLDDHMKVHKPKGVSEDCYINITYAPAHADTSSKLPVLMWF 144
QY 151 PGAFKTSASIFPGSALAAYEDVLVVVOYRLGIFGFTTMDQHPAGNMAFKQVALS 210
DB 145 PGAFKTSASIFPGSALAAYEDVLVVVOYRLGIFGFTTMDQHPAGNMAFKQVALS 204
QY 211 WVKNIIEFFGDPSSVITFGESAGASVSSLLSPMAKGLPHKAIMESGVAIIPYLBAND 270
DB 205 WVKNIIEFFGDPSSVITFGESAGASVSSLLSPMAKGLPHKAIMESGVAIIPYLBAND 264
QY 271 YEKSEDLQVNAHFCGNNADEBALRCLRTKPSKBLTLLSQTKTSFTTVVVGAFPPNEPL 330
DB 265 YEKSEDLQVNAHFCGNNADEBALRCLRTKPSKBLTLLSQTKTSFTTVVVGAFPPNEPL 324
QY 331 DLSOKAPKALPSITGVNNHSCGFLPKKEAPETLSGNSKSLAHLNLIHIPOYLH 390
DB 325 DLSOKAPKALPSITGVNNHSCGFLPKKEAPETLSGNSKSLAHLNLIHIPOYLH 384
QY 391 VANEYFHDKSLTELRDLDLGDVFFVVPALITARYHRDAGAVYEFYEFRRPOCED 450
DB 385 VANEYFHDKSLTELRDLDLGDVFFVVPALITARYHRDAGAVYEFYEFRRPOCED 444
QY 451 TKPAFVKADHDEVFVFGAFLKGDIMWFEGATEEEKLSRKKMKYATWATPARTGNPGN 510
DB 445 TKPAFVKADHDEVFVFGAFLKGDIMWFEGATEEEKLSRKKMKYATWATPARTGNPGN 504
QY 511 DLSLMPAYNLTEQYQLDLNLSLQRLKEPVDWMTSTIPILSLASDMLHSPSLSTPLS 570
DB 505 DLSLMPAYNLTEQYQLDLNLSLQRLKEPVDWMTSTIPILSLASDMLHSPSLSTPLS 564
QY 571 LLQPFPPFCAP 581
DB 565 LLQPFPPFCAP 575
RESULT 4

ADA54807
ID ADA54807 standard; protein; 525 AA.
XX
AC ADA54807;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human protein, SEQ ID 2375.
XX
KW Cytostatic; Anti-inflammatory; Osteoparic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX
OS Homo sapiens.
XX
PN EP1293569-A2.
XX
PD 19-MAR-2003.
XX
PF 21-MAR-2002; 2002EP-00006586.
XX
PR 14-SEP-2001; 2001JP-00328381.
XX 24-JAN-2002; 2002US-0350435P.
XX
PA (HELI-) HELIX RES INST.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
XX Seki N, Toshihara T, Otsuka M, Nagahara K, Masuho Y;
XX WPI; 2003-395339/38.
XX N-PSDB; ADA53168.
XX
PT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
XX Claim 14; SEQ ID NO 2375; 205pp; English.
XX
XX The present invention relates to novel human secretory or membrane
XX proteins (ADA54072-ADA55720) and their coding sequences (ADA52433-
XX ADA54071). The coding sequences are useful in the gene therapy of
XX diseases caused by abnormalities of the proteins, e.g. cancer,
XX inflammatory diseases, osteoporosis or neurological disease.
XX
XX Sequence 525 AA;
XX
Query Match 68.8%; Score 400; DB 6; Length 525;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 GPSAEGPQNRTRIGMIGKQVTVLGSFVNVFVGPAPRPGSRFTNPPQASPMDL 90
DB 25 GPSAEGPQNRTRIGMIGKQVTVLGSFVNVFVGPAPRPGSRFTNPPQASPMDL 84
QY 91 REATSYVNLCLQNSWMLLDQHLKHYKFGVSEDCLYNTYAPAHADTSGKLTVLWF 150
DB 85 REATSYVNLCLQNSWMLLDQHLKHYKFGVSEDCLYNTYAPAHADTSGKLTVLWF 144
QY 151 PGCAFRTGSAISIFDGSALAAEVDVLVWVQYRLGIFGFTTDOHAPGNMAFKQVALS 210
DB 145 PGCAFRTGSAISIFDGSALAAEVDVLVWVQYRLGIFGFTTDOHAPGNMAFKQVALS 204
QY 211 WYQKNIFFGGDPSSYTTIGESAGAISSVLLSPMAKGLFKKAIMESGVAIIPLYLHND 270
DB 205 WYQKNIFFGGDPSSYTTIGESAGAISSVLLSPMAKGLFKKAIMESGVAIIPLYLHND 264
QY 271 YKSEBDLQVVAHFCGNASDSBALRCLRTKPSKLLTLQKTKSFTTVVDGAFPEMPL 330
DB 265 YKSEBDLQVVAHFCGNASDSBALRCLRTKPSKLLTLQKTKSFTTVVDGAFPEMPL 324
QY 331 DLLSQAKFAIPISITIGVNNHECGFLLPMKEAPEILSGSNKSLALHLQNLILHIPPQYLH 390

DB 325 DLLSQAKFAIPISITIGVNNHECGFLLPMKEAPEILSGSNKSLALHLQNLILHIPPQYLH 384
QY 391 VANEYFHDKSLTEIRSLDLGADVFFVVPALITARYR 430
DB 385 VANEYFHDKSLTEIRSLDLGADVFFVVPALITARYR 424
RESULT 5
ABM84114
ID ABM84114 standard; protein; 642 AA.
XX
AC ABM84114;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4363.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic NM, Shen F,
PI Harshbarger TR, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve DL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitec UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patry S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
XX N-PSDB; ACN42766.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX in diagnosing a condition, disease or disorder associated with human
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
XX polynucleotide of the invention may have a use in gene therapy. The human
XX diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
XX used to diagnose a particular condition, disease or disorder associated
XX with human molecules, e.g. cell proliferative disorders,
XX autoimmune/inflammatory disorders, developmental disorders, endocrine
XX disorder, neurological disorders, gastrointestinal disorders, or
XX infections caused by virus, bacteria, fungi or parasite. The dthp
XX molecules may also be used in genetic mapping, in identifying individuals
XX from minute biological samples, in detecting single nucleotide
XX polymorphisms, as molecular weight markers, and for somatic or germline
XX gene therapy. The present sequence represents a dthp protein of the
XX invention. Note: The sequence data for this patent is not represented in
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at www.wipo.int/pct/en/sequences/1listing.htm
XX
XX Sequence 642 AA;
XX
Query Match 67.3%; Score 391; DB 8; Length 642;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 TMDQAPGNMAFKQVAAALSWQKNIIEFFGDPSSVTIFGSSAGAISSVSLTSPMAGL 250

DB 252 TMDQAPGNMAFKQVAAALSWQKNIIEFFGDPSSVTIFGSSAGAISSVSLTSPMAGL 311

QY 251 FHKAIMESGVAIIPYLEAHDEKSEDLQVVAHFCGNNAISDEALIRCLRTKPSKELLTUS 310

DB 312 FHKAIMESGVAIIPYLEAHDEKSEDLQVVAHFCGNNAISDEALIRCLRTKPSKELLTUS 371

QY 311 OKTSSFTVVGAFEPNPELDLSQAKFAIPSIIGVNNHEGFLPMKEAPEILISGSNK 370

DB 372 OKTSSFTVVGAFEPNPELDLSQAKFAIPSIIGVNNHEGFLPMKEAPEILISGSNK 431

QY 371 SLALHIONIILHIPPQYHLVANEYFHDKSHLSTEIRDSLLDGLGVFPVPLITARYHR 430

DB 432 SLALHIONIILHIPPQYHLVANEYFHDKSHLSTEIRDSLLDGLGVFPVPLITARYHR 491

QY 431 DAGAFVYFEPHRRPQCEFDTPKPAFVKADHAEVRFVFGAFLKGDIVMEGATEEKKL 490

DB 492 DAGAFVYFEPHRRPQCEFDTPKPAFVKADHAEVRFVFGAFLKGDIVMEGATEEKKL 551

QY 491 SRKMKYATPARKTPNGNDLSLMPAYNLTPQYIQLDNLNSLGRLEKPRDFTSTTP 550

DB 552 SRKMKYATPARKTPNGNDLSLMPAYNLTPQYIQLDNLNSLGRLEKPRDFTSTTP 611

QY 551 LILSADMLHSPSLTFLSLLOPPFFCAP 581

DB 612 LILSADMLHSPSLTFLSLLOPPFFCAP 642

RESULT 6
AAE25025
ID AAE25025 standard; protein; 642 AA.

XX AAE25025;
AC 30-OCT-2002 (first entry)
DT 30-OCT-2002 (first entry)
XX Human drug metabolizing enzyme (DME-10).
DE Human drug metabolizing enzyme (DME-10).
XX Human; drug metabolizing enzyme; autoimmune; inflammatory disorder;
KM acquired immunodeficiency syndrome; AIDS; atherosclerosis; psoriasis;
KM proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer;
KM asthma; neurological disorder; Alzheimer's disease; Huntington's disease;
KM dementia; Parkinson's disease; developmental disorder; anaemia; adenoma;
KM drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract;
KM renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer;
KM anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder;
KM goitre; gastrointestinal disorder; gene therapy; virulence; anticoagulant;
KM anticonvulsant; nootropic; enzyme; DME-10.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH 1..50
FT Peptide /label= Signal_peptide
FT 32..56
FT Domain /note= "Transmembrane domain"
FT /note= "Mature human DME-10"
FT 51..642
FT Protein 113..135
FT 135..145
FT Domain /note= "Transmembrane domain"
FT 204..220
FT Domain /note= "Transmembrane domain"
FT 234..250
FT Domain /note= "Transmembrane domain"
FT 287..314
FT Domain /note= "Transmembrane domain"
FT 463..491
FT Domain /note= "Transmembrane domain"
XX WO200246426-A2.

XX 13-JUN-2002.
PD 04-DEC-2001; 2001WO-US047429.
XX 08-DEC-2000; 2000US-0254308P.
XX 15-DEC-2000; 2000US-0256189P.
PR 21-DEC-2000; 2000US-0257713P.
PR 19-JAN-2001; 2001US-0262706P.
PR 02-FEB-2001; 2001US-0266020P.
XX (INCY-) INCYTE GENOMICS INC.
XX Sanjanwala MM, Yao MG, Au-Young J, Baughn MR, Arvizu C, Ring HZ,
PI Lee EA, Ding L, Hafalia AJA, Tang YT, Yue H, Tribouley CM, Lu DM,
PI Lal PG, Warren BA, Yang J, Walla NK, Nguyen DB, Gandhi AR, Lu Y,
PI Ison CH;
XX WPI: 2002-519668/55.
DR N-PSDB; AAD40574.
XX Novel human drug metabolizing polypeptide, useful in diagnosis,
PT prevention or treatment of autoimmune/inflammatory, cell proliferative,
PT neurological, developmental, endocrine, metabolic and gastrointestinal
PT disorders.
XX Claim 65; Page 155-156; 169pp; English.

XX The invention relates to an isolated human drug metabolizing enzyme (DME)
CC and its nucleotide. DME is useful for diagnosing, treating or preventing
CC disorders associated with aberrant expression of DME, where the disorders
CC are selected from autoimmune/inflammatory disorder such as acquired
CC immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis,
CC uveitis; a cell proliferative disorder such as arteriosclerosis,
CC cirrhosis, hepatitis, and cancer; a neurological disorder such as
CC Alzheimer's disease, Huntington's disease, dementia, Parkinson's disease;
CC a developmental disorder such as renal tubular acidosis, epilepsy,
CC anaemia; an endocrine disorder such as adenoma, thrombosis and infections
CC; an eye disorder such as conjunctivitis, glaucoma, cataract; metabolic
CC disorder such as cystic fibrosis, diabetes and goitre; a gastrointestinal
CC disorder such as anorexia, peptic ulcer; and liver disorders. DME is
CC useful in a number of drug screening techniques and to analyse the
CC proteome of a tissue or cell type. The invention is useful for creating
CC knock-in humanised animals or transgenic animals to model human diseases,
CC in somatic or germ-line gene therapy, to generate a transcript image of a
CC tissue or cell type, for detecting differences in the chromosomal
CC location due to translocation, inversion, etc. among normal, carrier or
CC affected individuals, and as hybridisation probes for mapping naturally
CC occurring genomic sequences. The present sequence is human DME-10
XX

Sequence 642 AA;

Query Match 65.6%; Score 381; DB 5; Length 642;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 31 GPSAEGPQRNRLGWIQGYVTLGSPVNVNVLGVPAAPIGLSLRTNPOPASPMNL 90

DB 92 GPSAEGPQRNRLGWIQGYVTLGSPVNVNVLGVPAAPIGLSLRTNPOPASPMNL 151

QY 91 REATSYPMICQNSEWMLLDQMLKVHPKFGVSEDCILYNIYAPAHADTGSKLPLVWF 150

DB 152 REATSYPMICQNSEWMLLDQMLKVHPKFGVSEDCILYNIYAPAHADTGSKLPLVWF 211

QY 151 PGAFKTSASIPDGSALAAVEDVLVNVQYRLGIFGFTTMDQAPGNMAFKQVAAAL 210

DB 212 PGAFKTSASIPDGSALAAVEDVLVNVQYRLGIFGFTTMDQAPGNMAFKQVAAAL 271

QY 211 WQKNIIEFFGDPSSVTIFGSSAGAISSVSLTSPMAGLPHKAIMESGVAIIPYLEAHD 270

DB 272 WQKNIIEFFGDPSSVTIFGSSAGAISSVSLTSPMAGLPHKAIMESGVAIIPYLEAHD 331

QY 271 YEKSEDLQVVAHFCGNNAISDEALIRCLRTKPSKELLTSLQKYSFTVVGAFEPNPEL 330

Db 332 YKSESDQVVAHFCGNNADESEALLRCLRTKPSKELLITTSQTKXSTFRVVDGAFPENEPL 391
 QY 331 DLSQKAFKAIPIIIGVNNHECGFLLPMKEAPEILSGNSKSLALHLIQLIHPQYLTL 390
 Db 392 DLSQKAFKAIPIIIGVNNHECGFLLPMKEAPEILSGNSKSLALHLIQLIHPQYLTL 451
 QY 391 VANEYFHDKSLTEIRDSLLDLDGDFVFPVPAITARYHRDAGAPYFPEFHRPQCFED 450
 Db 452 VANEYFHDKSLTEIRDSLLDLDGDFVFPVPAITARYHRDAGAPYFPEFHRPQCFED 511
 QY 451 TKRPFVKADHAEVRFVFGAFLKGDIVMEGATEBEKLSRKMKYATFARTGNPKN 510
 Db 512 TKRPFVKADHAEVRFVFGAFLKGDIVMEGATEBEKLSRKMKYATFARTGNPKN 571
 QY 511 DL 512
 Db 572 DL 573

RESULT 7
 ABP61006
 ID ABP61006 standard; protein; 356 AA.
 AC ABP61006;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Novel human protein. SEQ ID 93.
 XX
 KM Human; cytostatic; vulnary; antiatherosclerotic; antiparkinsonian;
 KM neurotropic; neuroprotective; immunosuppressive; haemostatic;
 KM antiinflammatory; cardiant; antitumor; virucide; antithyroid;
 KM cerebroprotective; anorectic; metabolic; Parkinson's disease;
 KM wound healing disorders; atherosclerosis; Parkinson's disease;
 KM Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
 KM inflammation; neoplastic disease; nervous system disorder;
 KM cardiovascular disorders; pancreatitis; respiratory disorder;
 KM hyperproliferation; systemic autoimmune disease; hyper-immunity;
 KM developmental abnormality; gastrointestinal ulceration; neuropathy;
 KM haematological disease; metabolic disease; sperm dysfunction;
 KM thyroid disorder; hypothyroidism; brain damage; colitis;
 KM cone photo-transduction deficiency; neurological disease; stroke;
 KM angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
 KM trachea; thymus; lymph node; muscular system; obesity; anorexia;
 KM growth abnormality; precocious puberty.
 KM
 XX Homo sapiens.
 OS
 XX
 PN WC000250105-A1.
 PD 27-JUN-2002.
 XX
 PF 17-DEC-2001; 2001MO-US049232.
 XX
 PR 19-DEC-2000; 2000US-0256710P.
 PR 20-DEC-2000; 2000US-0257048P.
 PR 09-JAN-2001; 2001US-0260482P.
 PR 30-JAN-2001; 2001US-0264922P.
 PR 06-FEB-2001; 2001US-0266797P.
 PR 19-MAR-2001; 2001US-0276988P.
 PR 04-APR-2001; 2001US-0281535P.
 PR 08-MAY-2001; 2001US-0289622P.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Agarwal P, Birkeland M, Cogswell JP, Kabnick KF, Lai Y,
 PI Marcensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q,
 XX WPI, 2002-508784/54.
 DR N-PSDB; ABQ86171.

XX Secreted proteins and polynucleotides useful as vaccines for preventing
 PT or treating various diseases e.g. cancer, wounds, atherosclerosis,
 PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
 XX
 PS Claim 1(a); Page 315; 335pp; English.

XX The invention relates to an isolated polypeptide with signal sequences
 CC which allow it to be secreted extracellularly or membrane associated. The
 CC activity of polypeptides of the invention may be described as,
 CC cytostatic, vulnary, antiatherosclerotic, antiparkinsonian, neurotropic,
 CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
 CC cardiant, antitumor, virucide, antithyroid, cerebroprotective, anorectic,
 CC and metabolic. Polypeptides and polynucleotides of the invention are
 CC useful in the treatment, or as a vaccine in the prevention of, cancer,
 CC wound healing disorders, infection, atherosclerosis, Parkinson's disease
 CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
 CC inflammation, neoplastic diseases, nervous system related disorders and
 CC cardiovascular disorders, systemic autoimmune disease, hyper-immunity,
 CC hyperproliferation, gastrointestinal ulceration, hyper-immunity,
 CC developmental abnormality, gastrointestinal ulceration, neuropathy,
 CC haematological diseases, metabolic diseases, sperm dysfunction, thyroid
 CC disorders e.g. hypothyroidism, brain damage, colitis, cone photo-
 CC transduction deficiency, neurological diseases, stroke, angiogenesis,
 CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
 CC trachea, thymus, lymph node and muscular system, obesity, anorexia,
 CC growth abnormalities, and alleviation of precocious puberty. The
 CC sequences given in records ABP60965-ABP61019 represent novel human
 CC proteins of the invention
 CC
 XX

SO Sequence 356 AA;

Query Match 58.5%; Score 340; DB 5; Length 356;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 ILSPAKLFLFKAIMESGVAIIPLYEAHDYKSSDLQVVAHFCGNNADESEALLRCLRTK 301
 Db 17 ILSPAKLFLFKAIMESGVAIIPLYEAHDYKSSDLQVVAHFCGNNADESEALLRCLRTK 76
 QY 302 PSKELLITTSQTKXSTFRVVDGAFPENEPLDLSQKAFKAIPIIIGVNNHECGFLLPMKEA 361
 Db 77 PSKELLITTSQTKXSTFRVVDGAFPENEPLDLSQKAFKAIPIIIGVNNHECGFLLPMKEA 136
 QY 362 PEILSGNSKSLALHLIQLIHPQYLHLVANEYFHDKSLTEIRDSLLDLDGDFVFPV 421
 Db 137 PEILSGNSKSLALHLIQLIHPQYLHLVANEYFHDKSLTEIRDSLLDLDGDFVFPV 196
 QY 422 ALITARYHRDAGAPYFPEFHRPQCFEDTKPAFVKADHAEVRFVFGAFLKGDIVMEF 481
 Db 197 ALITARYHRDAGAPYFPEFHRPQCFEDTKPAFVKADHAEVRFVFGAFLKGDIVMEF 256
 QY 482 GATEBEKLSRKMKYATFARTGNPKNGLSLMPAVNLTEOYLQDLNMSIGORLKEPR 541
 Db 257 GATEBEKLSRKMKYATFARTGNPKNGLSLMPAVNLTEOYLQDLNMSIGORLKEPR 316
 QY 542 VDFWTSITPILISASDMLHSPSSLTFLSLQPFPPFCAP 581
 Db 317 VDFWTSITPILISASDMLHSPSSLTFLSLQPFPPFCAP 356

RESULT 8
 ID ADB64065
 XX ADB64065 standard; protein; 469 AA.
 AC ADB64065;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human protein encoded by clone BRAWH20021910.
 XX
 KM Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
 KM cell regeneration; membrane protein; signal transduction-related protein;

XX	transcription-related protein; osteoporosis; neurological disease;
KW	Cancer; tumour.
OS	Homo sapiens.
XX	
PN	EPI308459-A2.
XX	
PD	07-MAY-2003.
XX	
PF	28-MAR-2002; 2002EP-00007401.
XX	
PR	05-NOV-2001; 2001JP-00379298.
PR	25-JAN-2002; 2002US-00350978.
XX	
PA	(HELI-) HELIX RES INST.
XX	(REAS-) RES ASSOC BIOTECHNOLOGY.
XX	
PI	Isozaki T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
PI	Seki N, Yoshikawa T, Otsuka M, Negahari K, Masuno Y,
XX	
DR	WPI; 2003-450961/43.
XX	
XX	N-PSDB; ADB62095.
PT	New polynucleotides and polypeptides, useful for developing a diagnostic
PT	marker or medicines for regulation of their expression and activity, or
PT	as targets of gene therapy.
XX	
PS	Claim 1; Page: 222pp; English.
XX	
CC	The invention discloses a polynucleotide comprising a sequence selected
CC	from 1970 fully defined nucleotide sequences which encode novel
CC	polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC	or its partial peptide, an antibody binding to the polypeptide or peptide
CC	of the polynucleotide, immunologically assaying the polypeptide or peptide
CC	with the antibody of the encoded protein, and observing the binding
CC	between the two, a transformant carrying the polynucleotide in an
CC	expressible manner and an antisense polynucleotide. The oligonucleotide
CC	is useful as a primer for synthesising the polynucleotide, or as a probe
CC	for detecting the polynucleotide. The polynucleotides and encoded
CC	proteins are useful as pharmaceutical agents and many disease-related
CC	genes may be included in them, for developing a diagnostic marker or
CC	medicines for regulation of their expression and activity, or as targets
CC	of gene therapy. The genes are involved in tissue and/or cell
CC	regeneration. Membrane proteins, signal transduction-related proteins,
CC	transcription-related proteins, disease-related proteins and genes
CC	encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC	neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC	the activity or expression of the encoded protein to treat diseases. The
CC	sequence presented is a protein of the invention. Note: Some of the
CC	sequence data for this patent is not represented in the printed
CC	specification, but is based on sequence information supplied by the
CC	European Patent Office.
XX	
XX	
SQ	Sequence 469 AA;
XX	
Query Match	56.6%; Score 329; DB 7; Length 469;
Best Local Similarity	99.8%; Pred. No. 8.5e-313;
Matches 429; Conservative	0; Mismatches 1; Indels 0; Gaps 0
QY	113 MLKVHYPRFVSEDCILYNIIVAPAHADTGSKLPLVLPWFGQAFKTSASIFDGSALAAVE 172
DB	1 MLKVHYPRFVSEDCILYNIIVAPAHADTGSKLPLVLPWFGQAFKTSASIFDGSALAAVE 60
QY	173 DVLVVVVVQVRIGIFGFFTTWDDHAPENMNAFKQVVALSWQKNIIEFGGDPSSVTIFGES 232
DB	61 DVLVVVVVQVRIGIFGFFTTWDDHAPENMNAFKQVVALSWQKNIIEFGGDPSSVTIFGES 120
QY	233 AGAIVSVSLILSPMAKGLFHKAKIMESGVAILPYLEAHADYEKSDLVVAHFCGNNAADSE 292
DB	121 AGAIVSVSLILSPMAKGLFHKAKIMESGVAILPYLEAHADYEKSDLVVAHFCGNNAADSE 180

QY	299	ALBRCRTPESEKLLTTSOKTCSFTRVVDGAFPNBPLDLLSQAFAPISIIIGVNNHCC	352
Db	181	ALBRCRTPESEKLLTTSOKTCSFTRVVDGAFPNBPLDLLSQAFAPISIIIGVNNHCC	240
QY	353	GFLLPKEAPELITSSGNSLSALHLIIONLHLPQYLHVNANEPHDSLTETIRDSILLDL	412
Db	241	GFLLPKEAPELITSSGNSLSALHLIIONLHLPQYLHVNANEPHDSLTETIRDSILLDL	300
QY	413	LGDFPVVVALITTAHYHDAGAPVYFYEFRRRPOCFBETKPAFPKADHADEVFVFGGAR	472
Db	301	LGDFPVVVALITTAHYHDAGAPVYFYEFRRRPOCFBETKPAFPKADHADEVFVFGGAR	360
QY	473	LKSDIMFEGATEEBEKLRSKKMKWAFPARTGPNNGNDLSLMPAYNLTEQYQLDLNMS	532
Db	361	LKSDIMFEGATEEBEKLRSKKMKWAFPARTGPNNGNDLSLMPAYNLTEQYQLDLNMS	420
QY	533	LGQRLKEPRV 542	
Db	421	LGQRLKEPRV 430	
RESULT 9			
ABP61005			
ID	ABP61005	standard; protein; 581 AA.	
XX	ABP61005;		
AC			
XX			
DT	10-SEP-2002	(first entry)	
XX			
DE	Novel human protein. SEQ ID 92.		
XX			
KM	Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian;		
KM	noctropic; neuroprotective; immunosuppressive; haemostatic;		
KM	antiinflammatory; cardiatic; antidiabetic; virucide; antithyroid;		
KM	cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;		
KM	wound healing disorders; atherosclerosis; Parkinson's disease;		
KM	Alzheimer's disease; autoimmune disorder; haematopoietic disorder;		
KM	inflammation; neoplastic disease; nervous system disorder;		
KM	cardiovascular disorders; pancreatitis; respiratory disorder;		
KM	hyperproliferation; systemic autoimmune disease; hyper-immunity;		
KM	developmental abnormality; gastrointestinal ulceration; neuropathy;		
KM	haematological disease; metabolic disease; sperm dysfunction;		
KM	thyroid disorder; hypothyroidism; brain damage; colitis;		
KM	cone photo-transduction deficiency; neurological disease; stroke;		
KM	angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;		
KM	trachea; thymus; lymph node; muscular system; obesity; anorexia;		
KM	growth abnormality; precocious puberty.		
XX			
OS	Homo sapiens.		
XX			
PN	MO200250105-A1.		
XX			
PD	27-JUN-2002.		
XX			
PF	17-DEC-2001; 2001MO-US049232.		
XX			
PR	19-DEC-2000; 2000US-0256710P.		
PR	20-DEC-2000; 2000US-0257048P.		
PR	09-JAN-2001; 2001US-0260482P.		
PR	30-JAN-2001; 2001US-0264922P.		
PR	06-FEB-2001; 2001US-0266797P.		
PR	19-MAR-2001; 2001US-0276988P.		
PR	04-APR-2001; 2001US-0281535P.		
PR	08-MAY-2001; 2001US-0289622P.		
XX			
PA	(SMIK) SMITHKLINE BEECHAM CORP.		
PA	(SMIK) SMITHKLINE BEECHAM PLC.		
PA	(GLAX) GLAXO GROUP LTD.		
XX			
XX			
PI	Agarwal P, Birkeland M, Cogswell JP, Kabnick KF, Lai Y;		
PI	Mattensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;		
XX			
DR	WPI; 2002-508784/54.		

DR N-PSDB; ABQ66170.
XX
PT Secreted proteins and polynucleotides useful as vaccines for preventing
PT or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
XX
XX Claim 1(a); Page 313-314; 335pp; English.
CC The invention relates to an isolated polypeptide with signal sequences
CC which allow it to be secreted extracellularly or membrane associated. The
CC activity of polypeptides of the invention may be described as,
CC cytostatic, vulnary, antiarteriosclerotic, antiparkinsonian, nootropic,
CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
CC cardiant, antitumor, vincristine, antithyroid, cerebroprotective, anorectic,
CC and metabolic. Polypeptides and polynucleotides of the invention are
CC useful in the treatment, or as a vaccine in the prevention of, cancer,
CC wound healing disorders, infection, atherosclerosis, Parkinson's disease
CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
CC inflammation, neoplastic diseases, nervous system related disorders and
CC cardiovascular disorders, pancreatitis, respiratory disorder.
CC hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC developmental abnormality, gastrointestinal ulceration, neuropathy,
CC haematological diseases, metabolic diseases, sperm dysfunction, thyroid
CC disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC transduction deficiency, neurological diseases, stroke, angiodenesis,
CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC growth abnormalities, and alleviation of precocious puberty. The
CC sequences given in records ABP0965-ABP61019 represent novel human
CC proteins of the invention
XX
SQ Sequence 581 AA;
Query Match 56.5%; Score 328; DB 5; Length 581;
Best Local Similarity 100.0%; Pred. No. 9,9e-312;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 GPSAEGPQNRRLTMIGQKQVTVLGSPPVAVFLGVPFAAPPLGSLRFTNPPQASPMNDL 90
Db 25 GPSAEGPQNRRLTMIGQKQVTVLGSPPVAVFLGVPFAAPPLGSLRFTNPPQASPMNDL 84
QY 91 REATSYPLCLQNSEMLLDQMLKVHPKRGVSEDCLYNTYAPAHADTGSRLPYLWVF 150
Db 85 REATSYPLCLQNSEMLLDQMLKVHPKRGVSEDCLYNTYAPAHADTGSRLPYLWVF 144
QY 151 PGAFKTSASIFDGSALAAVEDLVVVOYRLGIFGFTTMOHAGNNAFDDQVAALS 210
Db 145 PGAFKTSASIFDGSALAAVEDLVVVOYRLGIFGFTTMOHAGNNAFDDQVAALS 204
QY 211 WVOKNIEFGGDPSSVTTFESAGAISVSSLLISPAKGLFHKAIMESGVAIIPYLEAHD 270
Db 205 WVOKNIEFGGDPSSVTTFESAGAISVSSLLISPAKGLFHKAIMESGVAIIPYLEAHD 264
QY 271 YKSESDQVVAHFCGNNADEBALRLCTKPSKEILLTSQTKSTTRVVDGAFPPNEPL 330
Db 265 YKSESDQVVAHFCGNNADEBALRLCTKPSKEILLTSQTKSTTRVVDGAFPPNEPL 324
QY 331 DLISQAKFAKIPSIIGVNNHCEGFLPM 358
Db 325 DLISQAKFAKIPSIIGVNNHCEGFLPM 352
RESULT 10
ABU54639
ID ABU54639 standard; protein; 581 AA.
XX
XX ABU54639;
AC
XX
XX 03-JUN-2003 (first entry)
XX
XX Human NOVX polypeptide #98.
DE
XX
XX Human; NOVX; metabolic disorder; cardiomyopathy; diabetes; ASD;

KW hypertension; congenital heart defect; aortic stenosis; valve disease;
KW aortic septal defect; atriocentricular canal defect; ductus arteriosus;
KW pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD;
KW tubercular sclerosis; scleroderma; atherosclerosis; infectious disease;
KW obesity; anorexia; neurodegenerative disorder; Alzheimer's disease;
KW Parkinson's disease; immune disorder; haematopoietic disorder;
KW haemophilia; hypercoagulation; Crohn's disease; cancer.
XX
OS Homo sapiens.
XX
XX WO200281498-A2.
XX
XX 17-OCT-2002.
XX
XX 03-APR-2002; 2002WC-US010780.
XX
XX 03-APR-2001; 2001US-0281086P.
XX 03-APR-2001; 2001US-0281136P.
XX 05-APR-2001; 2001US-0281863P.
XX 05-APR-2001; 2001US-0281906P.
XX 06-APR-2001; 2001US-0282020P.
XX 10-APR-2001; 2001US-0282930P.
XX 10-APR-2001; 2001US-0282934P.
XX 12-APR-2001; 2001US-0283512P.
XX 13-APR-2001; 2001US-0283710P.
XX 17-APR-2001; 2001US-0284234P.
XX 19-APR-2001; 2001US-0285325P.
XX 20-APR-2001; 2001US-0285381P.
XX 20-APR-2001; 2001US-0285609P.
XX 23-APR-2001; 2001US-0285748P.
XX 23-APR-2001; 2001US-0285890P.
XX 24-APR-2001; 2001US-0286068P.
XX 25-APR-2001; 2001US-0286292P.
XX 27-APR-2001; 2001US-0287213P.
XX 02-MAY-2001; 2001US-0288257P.
XX 29-MAY-2001; 2001US-0294164P.
XX 30-MAY-2001; 2001US-0294484P.
XX 18-JUN-2001; 2001US-0298952P.
XX 19-JUN-2001; 2001US-0299237P.
XX 19-JUN-2001; 2001US-0299276P.
XX 12-SEP-2001; 2001US-0318750P.
XX 25-SEP-2001; 2001US-0324800P.
XX 25-SEP-2001; 2001US-0324802P.
XX 27-SEP-2001; 2001US-0325684P.
XX 17-OCT-2001; 2001US-0330143P.
XX 14-NOV-2001; 2001US-0332113P.
XX 14-NOV-2001; 2001US-0332240P.
XX 14-NOV-2001; 2001US-0332799P.
XX 21-NOV-2001; 2001US-0332115P.
XX 04-DEC-2001; 2001US-0337621P.
XX 03-JAN-2002; 2002US-0345783P.
XX 16-JAN-2002; 2002US-0350251P.
XX 02-APR-2002; 2002US-00114270.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Guo X. Kekuda R. Miller CE. Malyankar UM. Szytek KA;
XX Paturajan W. Liu X. Gusev VV. Li L. Vernet CAM. Zetunen BD;
XX Gorman L. Shenoy SG. Pena CE. Smithson G. Burgess CE. Gerlach V;
XX Padigaru M. Shimkets RA. Gangoli BA. Taupier RJ. Caeman SJ. Ji W;
XX Anderson DW. Leite MW. Rastelli L. Edinger SR. Stone DJ;
XX Macdougall JR. Rothenberg ME. Mazur A. Millet I. Feyman JA;
XX Ellerman K;
XX
XX WPI; 2003-046858/04.
XX
XX N-PSDB; ABX72267.
XX
XX
XX New isolated NOVX polypeptide useful for treating atherosclerosis,
XX metabolic disorders, diabetes, obesity, infectious disease, anorexia,
XX neurodegenerative disorders, Alzheimer's disease and cancer.
XX
XX Claim 1; Page 303; 666pp; English.

CC The invention relates to human polypeptides, termed NOV, and the
 CC polynucleotides encoding them. The polypeptides and polynucleotides are
 CC useful for diagnosing disease, and screening for potential therapeutic
 CC agents. The sequences are useful for treating metabolic disorders,
 CC cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic
 CC stenosis, atrial septal defect (ASD), atriocentricular canal defect,
 CC ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular
 CC septal defect (VSD), valve diseases, tuberculous sclerosis, scleroderma,
 CC atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative
 CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
 CC haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease
 CC and cancer. Sequences ABUS4542-ABUS4647 represent human NOVX polypeptides
 CC of the invention

CC Sequence 581 AA;

Query Match 56.5%; Score 328; DB 6; Length 581;
 Best Local Similarity 100.0%; Pred. No. 9.9e-312; Indels 0; Gaps 0;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GPSAGPQNRRLGWIQCKQVTVLSPVNVNVLGVPAPPLGSLRFTNPQASPMDNL 90
 DB 27 GPSAGPQNRRLGWIQCKQVTVLSPVNVNVLGVPAPPLGSLRFTNPQASPMDNL 86
 QY 91 REATSYPNLCLQNSEWMLLDQHLKVRYPKGVSEDCLYLNIYAPAHADTGSKLPVLWVF 150
 DB 87 REATSYPNLCLQNSEWMLLDQHLKVRYPKGVSEDCLYLNIYAPAHADTGSKLPVLWVF 146
 QY 151 PGGAFTGSSASIFDSSALAAVEDVAVVVOYRLGIFGFTTWDQAPGNMAFKDQVAALS 210
 DB 147 PGGAFTGSSASIFDSSALAAVEDVAVVVOYRLGIFGFTTWDQAPGNMAFKDQVAALS 206
 QY 211 WVKQNIIEFGDPSVTFIAGESAGAISSVSLILSPMAKGLFKAIMESGVAIIPYLEAHD 270
 DB 207 WVKQNIIEFGDPSVTFIAGESAGAISSVSLILSPMAKGLFKAIMESGVAIIPYLEAHD 266
 QY 271 YEKSEDLQVVAHFCGNNADESEALLRCLRTKPSKELLTLISOKTGSFTRVVDGAFPPNEPL 330
 DB 267 YEKSEDLQVVAHFCGNNADESEALLRCLRTKPSKELLTLISOKTGSFTRVVDGAFPPNEPL 326
 QY 331 DLSQAKFAKAIPIIIGVNNHCEGFLPM 358
 DB 327 DLSQAKFAKAIPIIIGVNNHCEGFLPM 354

RESULT 11

ADRI9663 standard; protein; 618 AA.

ADRI9663;

07-OCT-2004 (first entry)

Human drug metabolizing enzyme (DME)-2 protein sequence.

XX drug metabolizing enzyme; DME; cytosolic; immunosuppressive;
 XX antiinflammatory; endocrine; ophthalmological; gastrointestinal;
 XX hepatotropic; cancer; cell proliferative disorder; autoimmune disorder;
 XX inflammatory disorder; endocrine disorder; eye disorder;
 XX gastrointestinal disorder; liver disorder; metabolic disorder; enzyme;
 XX human.

OS Homo sapiens.

PN WO200226988-A2.

PD 04-APR-2002.

PF 28-SEP-2001; 2001WO-US030662.

PR 29-SEP-2000; 2000US-0236947P.

PR 06-OCT-2000; 2000US-0238664P.

PR 20-OCT-2000; 2000US-0242323P.

PR 09-NOV-2000; 2000US-0247581P.
 PR 16-NOV-2000; 2000US-0249519P.
 PR 22-NOV-2000; 2000US-0252834P.
 PR 30-NOV-2000; 2000US-0250567P.

(INCYTE GENOMICS INC.

XX Azimzai Y, Baughin MR, Borowsky ML, Ding L, Duggan BM,
 PI Elliott VS, Gandhi AR, Griffin JA, Hafalia AJA, Ison CH, Khan FA,
 PI Lal P, Lee BA, Lu DAM, Nguyen DB, Arvizu C, Policky JL, Ramkumar J;
 PI Ring HZ, Sanjanwala MS, Tang YT, Tribouley CM, Narinder WK;
 PI Walsh RT, Warren BA, Xu Y, Yang J, Yao MG, Yue H;

XX WPI; 2002-362498/39.

DR N-PSDB; ADRI9681.

PT Human drug metabolizing enzymes, useful in the diagnosis and treatment of
 PT disorders associated with aberrant (DME) activity, e.g., cancer and
 PT autoimmune disorders.

PS Claim 1; SEQ ID NO 2; 142bp; English.

CC This invention relates to novel drug metabolizing enzymes (DME) and the
 CC nucleotide sequences which encode them. The invention may be useful for
 CC the development of compounds with a cytosolic, immunosuppressive,
 CC antiinflammatory, endocrine, ophthalmological, gastrointestinal or
 CC hepatotropic activity acting as an agonist or antagonist of drug
 CC metabolizing enzyme activity. The invention may be used in the diagnosis
 CC and treatment of disorders associated with decreased or increased
 CC expression or activity of drug metabolizing enzymes. Such disorders
 CC include cancer, cell proliferative disorders, autoimmune/inflammatory,
 CC endocrine, eye, gastrointestinal (including liver disorders) and
 CC metabolic disorders. The present sequence is that of a human drug
 CC metabolizing enzyme (DME) of the invention. Note: This sequence did not
 CC form part of the printed specification but was obtained in electronic
 CC format from EPO.

CC Sequence 618 AA;

Query Match 56.5%; Score 328; DB 5; Length 618;
 Best Local Similarity 100.0%; Pred. No. 1.1e-311; Indels 0; Gaps 0;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GPSAGPQNRRLGWIQCKQVTVLSPVNVNVLGVPAPPLGSLRFTNPQASPMDNL 90
 DB 92 GPSAGPQNRRLGWIQCKQVTVLSPVNVNVLGVPAPPLGSLRFTNPQASPMDNL 151
 QY 91 REATSYPNLCLQNSEWMLLDQHLKVRYPKGVSEDCLYLNIYAPAHADTGSKLPVLWVF 150
 DB 152 REATSYPNLCLQNSEWMLLDQHLKVRYPKGVSEDCLYLNIYAPAHADTGSKLPVLWVF 211
 QY 151 PGGAFTGSSASIFDSSALAAVEDVAVVVOYRLGIFGFTTWDQAPGNMAFKDQVAALS 210
 DB 212 PGGAFTGSSASIFDSSALAAVEDVAVVVOYRLGIFGFTTWDQAPGNMAFKDQVAALS 271
 QY 271 WVKQNIIEFGDPSVTFIAGESAGAISSVSLILSPMAKGLFKAIMESGVAIIPYLEAHD 270
 DB 272 WVKQNIIEFGDPSVTFIAGESAGAISSVSLILSPMAKGLFKAIMESGVAIIPYLEAHD 331
 QY 271 YEKSEDLQVVAHFCGNNADESEALLRCLRTKPSKELLTLISOKTGSFTRVVDGAFPPNEPL 330
 DB 332 YEKSEDLQVVAHFCGNNADESEALLRCLRTKPSKELLTLISOKTGSFTRVVDGAFPPNEPL 391
 QY 331 DLSQAKFAKAIPIIIGVNNHCEGFLPM 358
 DB 392 DLSQAKFAKAIPIIIGVNNHCEGFLPM 419

RESULT 12

ADCS5524 standard; protein; 224 AA.

ADCS5524;

XX 06-NOV-2001 (first entry)
XX Human polypeptide SEQ ID NO 19709.
DE
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation.
OS Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US004927.
XX
XX 28-FEB-2000; 2000US-00515126.
XX 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Dermanac RT;
XX
XX MPI; 2001-514838/56.
XX N-PSDB; AA185748.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 20; SEQ ID NO 19709; 1399bp + Sequence listing; English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
XX the encoded proteins (AA000010-AA013910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 124 AA;
SQ
Query Match 9.5%; Score 55; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 4.7e-45;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 449 EDTKPAFYKADHAEVRFVFGAPFLKGDIVMEGATEEBEKLSSROMKYMATFAR 503
DB 20 EDTKPAFYKADHAEVRFVFGAPFLKGDIVMEGATEEBEKLSSROMKYMATFAR 74
RESULT 15
ID AAE20909 standard; protein; 306 AA.
XX AAE20909;
XX
XX AAE20909;
XX
XX 01-JUL-2002 (first entry)
XX
XX Human carboxylesterase-like enzyme protein #1.
DE
XX Human; carboxylesterase-like enzyme; organophosphorus intoxication;
XX osteoporosis; gene therapy; osteoporosis; antitense therapy; cytostatic;
XX detoxifying agent; Paget's disease; bone implant degradation; cancer;
XX dental implant; enzyme; gene expression.
XX

OS Homo sapiens.
XX
XX WO200206454-A2.
XX
XX 24-JAN-2002.
XX
XX 10-JUL-2001; 2001WO-EP007919.
XX
XX 17-JUL-2000; 2000US-0218564P.
XX
XX (FARB) BAYER AG.
XX
XX Xiao Y;
XX
XX MPI; 2002-195808/25.
XX N-PSDB; AAD33344.
XX
XX Novel human carboxylesterase-like enzyme polypeptide, regulators of which
XX are useful for preventing and treating organophosphorus intoxication,
XX cancer and osteoporosis.
XX
XX Claim 25; Fig 5; 92bp; English.
XX
XX The invention relates to a purified human carboxylesterase-like enzyme
XX polypeptide. Carboxylesterase-like enzyme and its DNA are useful for
XX screening for agents which decrease or modulate the activity of
XX carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is
XX useful for treating a carboxylesterase-like enzyme dysfunction related
XX disease, such as organophosphorus intoxication, cancer and osteoporosis.
XX Compounds that increase the ability of human carboxylesterase-like enzyme
XX to bind to organophosphorus compounds are useful as detoxifying agents.
XX Carboxylesterase-like enzyme agonists and antagonists are useful for
XX treating osteoporosis, Paget's disease and degradation of bone implants,
XX particularly dental implants. Carboxylesterase-like enzyme is useful in
XX diagnostic assays for detecting diseases and abnormalities or
XX susceptibility to diseases or abnormalities related to the presence of
XX mutations in the nucleic acid sequences which encode the enzyme. The
XX coding sequence of carboxylesterase-like enzyme polynucleotide is useful
XX in gene therapy and for generating antisense oligonucleotides or
XX ribozymes which specifically bind to mRNA transcribed from
XX carboxylesterase-like enzyme DNA. These antisense oligonucleotides are
XX useful for modulating carboxylesterase-like enzyme gene expression. The
XX present sequence is human carboxylesterase-like enzyme protein
XX
XX Sequence 306 AA;
SQ
Query Match 9.3%; Score 54; DB 5; Length 306;
Best Local Similarity 100.0%; Pred. No. 1e-43;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 179 VOYRIGTGFPTTMDQAHAGMAMFQDVAALSWQKNIFFGDPSSVTIRGES 232
DB 53 VOYRIGTGFPTTMDQAHAGMAMFQDVAALSWQKNIFFGDPSSVTIRGES 106
RESULT 16
ID ABG66757 standard; protein; 84 AA.
XX ABG66757;
XX
XX 30-AUG-2002 (first entry)
XX
XX Human novel polypeptide #92.
DE
XX Human; inflammatory condition; shock; sepsis; immune response; cancer;
XX wound healing; central nervous system disease; haematopoiesis;
XX peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
XX myofibril cell disorder; lymphoid cell disorder; platelet disorder; bone;
XX cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
XX bone degenerative disorder; periodontal disease; reperfusion injury;
XX lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
XX allergic condition; thrombolysis; thrombosis; coagulation disorder;
XX

KW fungal infection.
XX
OS Homo sapiens.
XX
PN MO200244340-A2.
XX
PD 06-JUN-2002.
XX
PF 30-NOV-2001; 2001MO-US047004.
XX
PR 30-NOV-2000; 2000US-00728952.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YF, Goodrich RM, Liu C, Zhou P, Asundi V, Wang J, Wang D,
PI Yamazaki V, Ujwal ML, Drmanac RT;
XX WPI, 2002-508509/54.
DR N-PSDB; ABR94981.
XX
PT Novel nucleic acids and polypeptides for diagnosis, treatment of
PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
PT disorders, cancer and promoting wound healing.
XX
PS Claim 10; Page 672; 672pp; English.
XX
CC The invention relates to human novel polynucleotides and associated
CC polypeptides. The polynucleotides and polypeptides are useful for
CC treating inflammatory conditions such as arthritis, nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
CC and cancer and for promoting wound healing. The sequences are used to
CC induce the proliferation of neural cells and regeneration of nerve and
CC brain tissue, and are useful for the treatment of central and peripheral
CC nervous system diseases and neuropathies, such as Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and amyotrophic lateral
CC sclerosis. The sequences are involved in chemotactic or chemokinetic
CC activity, regulation of hematopoiesis, treatment of myeloid or lymphoid
CC cell disorders and platelet disorders such as thrombocytopenia,
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
CC disease. The sequences of the invention are also useful for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, immune deficiencies and disorders
CC including severe combined immunodeficiency (SCID), bacterial or fungal
CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia
CC gravis, allergic conditions such as asthma, thrombolytic or thrombotic
CC and coagulation disorders. Sequences ABR66666-ABR66758 represent human
CC novel polypeptides of the invention
XX
SQ Sequence 84 AA;
Query Match 8.8%; Score 51; DB 5; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 179 VQYRLGIFGFTTWDQHPGNNAFKDQVALSVQKNIEFGDPSSVTIF 229
DB 6 VQYRLGIFGFTTWDQHPGNNAFKDQVALSVQKNIEFGDPSSVTIF 56
RESULT 17
AAM16665
ID AAM16665 standard; protein; 49 AA.
XX
AC AAM16665;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #3099 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.

XX
OS Homo sapiens.
XX
PN MO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001MO-US000670.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI, 2001-488901/53.
XX
DR
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX
PS Claim 27; SEQ ID NO 21491; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SEN; see A110068-A118459). The present sequence is a peptide encoded
CC by one such probe. The SENs are derived from human HeLa cells. The SENs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at http://wipo.int/pub/published_pct_sequences
XX
SQ Sequence 49 AA;
Query Match 8.4%; Score 49; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 432 AGAPVYFEYFRHRPQCEBDTTPAFVKADHDEVRFVFGAFLKGDIVMF 480
DB 1 AGAPVYFEYFRHRPQCEBDTTPAFVKADHDEVRFVFGAFLKGDIVMF 49
RESULT 18
ABR35649
ID ABR35649 standard; peptide; 49 AA.
XX
AC ABR35649;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #3155 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN MO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001MO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
XX
XX Claim 27; SEQ ID NO 28284; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 49 AA;

Query Match 8.4%; Score 49; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 432 AGAIVYEFEPHRRPOCFEDTKPAFVKADHAEVRFVFGAFLKGDIVMF 480
Db 1 AGAIVYEFEPHRRPOCFEDTKPAFVKADHAEVRFVFGAFLKGDIVMF 49

RESULT 19
ID AAM29149 standard; protein; 49 AA.
XX
AC AAM29149;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #1186 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.

XX
XX Claim 27; SEQ ID NO 29418; 654pp; English.
XX
XX
XX The present invention relates to single exon nucleic acid probes (SENP:
CC see A113115-A157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 49 AA;

Query Match 8.4%; Score 49; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 432 AGAIVYEFEPHRRPOCFEDTKPAFVKADHAEVRFVFGAFLKGDIVMF 480
Db 1 AGAIVYEFEPHRRPOCFEDTKPAFVKADHAEVRFVFGAFLKGDIVMF 49

RESULT 20
ID ABB30482 standard; peptide; 49 AA.
XX
AC ABB30482;
XX
DT 01-FEB-2002 (first entry)
XX
DE Peptide #1133 encoded by breast cell single exon nucleic acid probe.
XX
XX Human; microarray; single exon probe; gene expression; breast; disease;
XX cancer.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000662.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.
XX
XX Claim 27; SEQ ID NO 13450; 327pp + Sequence Listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting the
CC probes with a collection of detectably labeled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode proteins. They
CC are useful for gene discovery, and for determining predisposition and/or
CC prognosing breast disease. Gene expression analysis is useful for
CC assessing the toxicity of chemical agents on cells. The microarray of
CC this invention presents a far greater diversity of probes for measuring

CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a peptide
CC encoded by a single exon nucleic acid probe of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 49 AA;

Query Match 8.4%; Score 49; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 AGAPVYFEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFLKGDIVMF 480
DB 1 AGAPVYFEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFLKGDIVMF 49

RESULT 21

ABB21078
ID ABB21078 standard; protein; 49 AA.

XX ABB21078;

DT 23-JAN-2002 (first entry)

DE Protein #3077 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease.

OS Homo sapiens.

XX WO200157274-A2.

PN 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000666.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX hearts.

XX Claim 15; SEQ ID NO 22848; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX By measuring gene expression, the probes are useful for predicting,
XX diagnosing, grading, staging, monitoring and prognosing diseases of the
XX human heart and vascular system e.g. cardiovascular disease,
XX hypertension, cardiac arrhythmias and congenital heart disease. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences

SEQ Sequence 49 AA;

Query Match 8.4%; Score 49; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 AGAPVYFEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFLKGDIVMF 480
DB 1 AGAPVYFEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFLKGDIVMF 49

RESULT 22

AAM68842
ID AAM68842 standard; protein; 49 AA.

XX AAM68842;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 29148.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.

XX Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human bone marrow.

XX Example 4; SEQ ID NO 29148; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX bone marrow. They can be used to measure gene expression in bone marrow

XX samples, which may enable the improved diagnosis and treatment of cancers

XX such as lymphoma, leukaemia and myeloma. The present sequence is a

XX protein encoded by one of the probes of the invention

XX Sequence 49 AA;

Query Match 8.4%; Score 49; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.5e-39;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 AGAPVYFEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFLKGDIVMF 480
DB 1 AGAPVYFEFRHRPQCFEDTKPAFVKADHDEVRFVFGAFLKGDIVMF 49

RESULT 23

AAM56465
ID AAM56465 standard; protein; 49 AA.

XX

```

AC AAM56465;
XX
XX 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28570.
XX
XX Human; brain expressed exon; gene expression analysis; probe: microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Example 4; SEQ ID NO 28570; 650bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancer. The present sequence is a protein encoded by one of
XX the probes of the invention
XX
XX Sequence 49 AA;
XX
XX Query Match 8.4%; Score 49; DB 4; Length 49;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-39;
XX Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 432 AGAPVYFEFRRHRCQCFEDTKPAFYKADHADVRFVFGAFLKGDIVMF 480
XX 1 AGAPVYFEFRRHRCQCFEDTKPAFYKADHADVRFVFGAFLKGDIVMF 49
XX
XX RESULT 24
XX ID AAG50502
XX ABG50502 standard; peptide; 49 AA.
XX
XX AC ABG50502;
XX
XX 25-FEB-2003 (first entry)
XX
XX Human liver peptide, SEQ ID NO 29150.
XX
XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX hypercholesterolaemia; coronary heart disease.
XX
XX Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX

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XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 27; SEQ ID NO 29150; 658bp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABG47348-ABG59930 represent human
XX liver single exon encoded peptides of the invention. Note: The sequence
XX information for this patent does not appear in the printed specification
XX but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 49 AA;
XX
XX Query Match 8.4%; Score 49; DB 4; Length 49;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-39;
XX Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 432 AGAPVYFEFRRHRCQCFEDTKPAFYKADHADVRFVFGAFLKGDIVMF 480
XX 1 AGAPVYFEFRRHRCQCFEDTKPAFYKADHADVRFVFGAFLKGDIVMF 49
XX
XX RESULT 25
XX ID AAM04381
XX AAM04381 standard; protein; 49 AA.
XX
XX AC AAM04381;
XX
XX 09-OCT-2001 (first entry)
XX
XX Peptide #3063 encoded by probe for measuring breast gene expression.
XX
XX Probe; human; breast disease; breast cancer; development disorder;
XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
XX Homo sapiens.
XX
XX WO200157270-A2.
XX
XX 09-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US000661.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX

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21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2002-476286/51.
 XX
 PT Novel single exon nucleic acid probe used to measuring gene expression in
 PT a human breast.
 XX
 PS Claim 27; SEQ ID NO 13121; 322pp; English.
 XX
 CC The present invention relates to novel single exon nucleic acid probes
 CC (see A100010-A110067). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for measuring human gene expression in
 CC a human breast sample, where the probe hybridizes at high stringency to a
 CC nucleic acid expressed in the human breast. The probes are useful for
 CC predicting, diagnosing, grading, staging, monitoring and prognosing
 CC diseases of the human breast, particularly those diseases with polygenic
 CC inflammatory diseases of the breast, breast cancer, disorders of development,
 CC breast disease and non-carcinoma tumours. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WPI at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 49 AA;
 XX
 QY
 Query Match 8.4%; Score 49; DB 4; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.5e-39;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 ID 432 AGAPVYFEEFRHRPQCFEDTKPAFYKADHADVRFVFGAFLKGDIVWF 480
 DB 1 AGAPVYFEEFRHRPQCFEDTKPAFYKADHADVRFVFGAFLKGDIVWF 49
 XX
 RESULT 26
 ABG38423
 ID ABG38423 standard; peptide; 49 AA.
 XX
 AC ABG38423;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 28088.
 XX
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200186003-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000665.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456E.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2002-114183/15.
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 PS Claim 27; SEQ ID NO 28088; 634pp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC ; the novel set of probes which hybridize at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung; comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA; and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridization of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarray having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, lymphangioleiomyomatosis, pulmonary haemosiderosis,
 CC histiocytosis, pulmonary hypertension and hyaline membrane disease. The
 CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WPI at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 49 AA;
 XX
 QY
 Query Match 8.4%; Score 49; DB 5; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.5e-39;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 ID 432 AGAPVYFEEFRHRPQCFEDTKPAFYKADHADVRFVFGAFLKGDIVWF 480
 DB 1 AGAPVYFEEFRHRPQCFEDTKPAFYKADHADVRFVFGAFLKGDIVWF 49
 XX
 RESULT 27
 AA20912
 ID AA20912 standard; peptide; 41 AA.
 XX
 AC AA20912;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Carboxylesterase type-B serine peptide #1.

```
FN XX JP2003250575-A.  
XX PD  
XX 09-SEP-2003.  
PE PF 04-MAR-2002; 2002JP-00057908.  
PR XX 04-MAR-2002; 2002JP-00057908.  
XX PA (TOHO-) TOHOKU TECHNOARCH KK.  
XX WPI; 2004-002277/01.  
DR N-PSDB; ADF50144.  
PT Novel cauxin protein or its salt, useful as a cat kidney disease marker,  
XX and for diagnosing cat kidney disease.  
XX PS Claim 3; SEQ ID NO 2; 33bp; Japanese.  
XX The present sequence represents a cat cauxin protein (I) or its salt,  
CC which is cat kidney disease marker. Also described: (1) a partial peptide  
CC (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector  
CC (IV) comprising (III); (4) a transformed host (V) comprising (III) or  
CC (IV); (5) producing (I) or (II) by culturing (V); (6) an antibody (VI)  
CC which comprises specifically with (I) or (II); (7) diagnosing cat kidney  
CC disease which involves measuring (I) quantitatively, and where reduction  
CC of amount of (I) indicates presence of the disease; (8) a cat kidney  
CC disease diagnostic agent comprising (I) labelling agent, a reagent which  
CC measures the biological activity of urinary (I) or (VI); and (9) a cauxin  
CC detection kit which measures cauxin in a test sample. (I) is useful as a  
CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney  
CC disease. (I) enables detection of cat kidney disease simply and  
CC correctly. (I) provides an early marker for the disease, and replaces  
CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,  
CC blood testing.  
SQ Sequence 542 AA;  
  
Query Match 5.3%; Score 31; DB 8; Length 542;  
Best Local Similarity 100.0%; Pred. No. 5.9e-21;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 465 RFVGGAFLKGDIVMEFGATEBEETLSRKMM 495  
| | | | |  
Db 456 RFVGGAFLKGDIVMEFGATEBEETLSRKMM 486  
| | | | |  
  
RESULT 29  
ADFS0147  
ID ADFS0147 standard; protein; 542 AA.  
AC ADFS0147;  
XX AD FS0147;  
DT 12-FEB-2004 (first entry)  
DE Cat cauxin protein SEQ ID NO:4.  
XX cat; cauxin; cat kidney disease marker; kidney disease.  
OS Felis catus.  
XX JF2003250575-A.  
PN PN  
PD 09-SEP-2003.  
PF 04-MAR-2002; 2002JP-00057908.  
PR 04-MAR-2002; 2002JP-00057908.  
XX (TOHO-) TOHOKU TECHNOARCH KK.  
XX WPI; 2004-002277/01.  
DR N-PSDB; ADFS0146.
```

XX Novel cauxin protein or its salt, useful as a cat kidney disease marker,
PT and for diagnosing cat kidney disease.
XX
XX
PS Disclosure; SEQ ID NO 4; 33pp; Japanese.
XX

CC The present sequence represents a cat cauxin protein (I) or its salt,
CC which is cat kidney disease marker. Also described: (1) a partial peptide
CC (II) of (I); (2) a nucleic acid (II) encoding (I) or (II); (3) a vector
CC (IV) comprising (III); (4) a transformed host (V) comprising (III) or
CC (IV); (5) producing (I) or (II) by culturing (V); (6) an antibody (VI)
CC which couples specifically with (I) or (II); (7) diagnosing cat kidney
CC disease which involves measuring (I) quantitatively, and where reduction
CC of amount of (I) indicates presence of the disease; (8) a cat kidney
CC disease diagnostic agent comprising (I) labelling agent, a reagent which
CC measures the biological activity of urinary (I) or (VI); and (9) a cauxin
CC detection kit which measures cauxin in a test sample. (I) is useful as a
CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney
CC disease. (I) enables detection of cat kidney disease simply and
CC correctly. (I) provides an early marker for the disease, and replaces
CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,
CC blood testing.
XX

XX Sequence 542 AA;

Query Match 5.3%; Score 31; DB 8; Length 542;
Best Local Similarity 100.0%; Pred. No. 5.9e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 465 RFVFGAFLKGDIVWFEGATEEKLISRKM 495
|||
DB 456 RFVFGAFLKGDIVWFEGATEEKLISRKM 486

Search completed: June 16, 2005, 21:01:29
Job time : 171 secs

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OM protein - protein search, using sw model

Run on: June 16, 2005, 20:46:43 ; Search time 42 Seconds
(without alignments)
1330.999 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 581
Sequence: 1 MPQGLTSSASQWCFPLIQP.....PLSLTFLSLIQPFFFCAP 581

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 30

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
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No matches found

Search completed: June 16, 2005, 21:02:15
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2005, 20:54:53 ; Search time 180 Seconds
(without alignments)
1652.878 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 581
Sequence: 1 MPOGITSASQWCFLLIQP.....PLSSITFLSLQPPFFFCAP 581

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 30

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trernbl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	94.8	575	2	Q6NTJ32
2	400	68.8	525	2	Q96DN9
3	329	56.6	469	2	Q8NBC8
4	101	17.4	361	2	Q95KH3
5	31	5.3	545	2	Q81034

ALIGNMENTS

RESULT 1
Q6NTJ32 PRELIMINARY; PRT; 575 AA.
AC Q6NTJ32: 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE FLJ31547 protein.
GN Name=FLJ31547;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242601899;
RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schneitz T.E.,
RA Brownstein M.J., Uedini T.B., Toshitsuki S., Carantini P., Prange C.,
RA Rana S.S., Loguigliano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
RA Boak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schermer A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Director MGC Project;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL: BC069501; AAH69501.1; -.
DR HSBP: P12337; IK4Y.
DR GO: GO:0003824; F:catalytic activity; IEA.
DR InterPro: IPR002018; Carboxylesterase.
DR InterPro: IPR003179; Ser estase.
DR Pfam: PF00135; Coesterase; 1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
DR KW Hydrolase.
SQ SEQUENCE 575 AA; 63926 MW; 6F5B735BDEFC9C09 CRC64;

Query Match 94.8%; Score 551; DB 2; Length 575;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 GPSAEGPQNRNRLGWIQKQVTVLSPVNVVFLGPPAPPLGSLRFTNPQAPSPMDL 90
DB 25 GPSAEGPQNRNRLGWIQKQVTVLSPVNVVFLGPPAPPLGSLRFTNPQAPSPMDL 84
QY 91 REATSYPLCLQNSSEWLLDQMLKVPKPGVSEDCLYNIYAPAHADTSGKLPVWVF 150
DB 85 REATSYPLCLQNSSEWLLDQMLKVPKPGVSEDCLYNIYAPAHADTSGKLPVWVF 144
QY 151 PGGAFTGSASITPDGSALAAVEDLVVVVQYRLGIFGFTTWDQAPGNMAFKQVAALS 210
DB 145 PGGAFTGSASITPDGSALAAVEDLVVVVQYRLGIFGFTTWDQAPGNMAFKQVAALS 204
QY 211 WYQKNIIEFGDPSVTIFGESAGAIYSVSLILSPMAKGLFKHAKIMESGVAIIPYLEAHD 270
DB 205 WYQKNIIEFGDPSVTIFGESAGAIYSVSLILSPMAKGLFKHAKIMESGVAIIPYLEAHD 264
QY 271 YEKSEDLQVVAHFCGNNADEBALLRCLRTKPSKELLTLISQKTSFTRVVDGAPFPNPL 330
DB 265 YEKSEDLQVVAHFCGNNADEBALLRCLRTKPSKELLTLISQKTSFTRVVDGAPFPNPL 324
QY 331 DLSLQKAKAIPSIIGVNNHCGFLIPMKKAPELLISGNKSLAHLIQLIHIIPQYVHL 390
DB 325 DLSLQKAKAIPSIIGVNNHCGFLIPMKKAPELLISGNKSLAHLIQLIHIIPQYVHL 384
QY 391 VANEYFFHKSILTEIRDSLLDLGDVFPVVPALITARHRODGAQVYFEYFRHRQCFED 450
DB 385 VANEYFFHKSILTEIRDSLLDLGDVFPVVPALITARHRODGAQVYFEYFRHRQCFED 444
QY 451 TKPAFVKADHAEVAFVVGGAFLKGDIVMEFGATEEEXLRSKMKKYATFARTGNPKN 510
DB 445 TKPAFVKADHAEVAFVVGGAFLKGDIVMEFGATEEEXLRSKMKKYATFARTGNPKN 504
QY 511 DLSLQKAKAIPSIIGVNNHCGFLIPMKKAPELLISGNKSLAHLIQLIHIIPQYVHL 570
DB 505 DLSLQKAKAIPSIIGVNNHCGFLIPMKKAPELLISGNKSLAHLIQLIHIIPQYVHL 564

OY 571 LLOPFFPCAP 581
 Db 565 LLOPFFPCAP 575

RESULT 2

096DN9 PRELIMINARY; PRT; 525 AA.
 AC 096DN9; ID 096DN9; DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein FLJ151547.
 GN Name=FLJ151547;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahata K.,
 Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 Niimiya K., Ishihashi T., Yamashita H., Murakawa K., Fujimori K.,
 Tanai H., Kimura M., Watanabe M., Hirano S., Chiba Y., Iehida S.,
 Ono Y., Takiguchi S., Watanabe M., Hirano S., Chiba Y., Iehida S.,
 Kanohori K., Takahashi-Fujii A., Hara H., Tanase T., Kusano J.,
 Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 Musughino K., Yuki H., Oshima H., Sasaki N., Aotaka S.,
 Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 Hishigaki H., Watanabe K., Sugiyama A., Takemoto M., Kakikami B.,
 Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujizawa T.,
 Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 Miushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 Okumura K., Nagase T., Nomura N., Kikuchi H., Maehou Y., Yamashita R.,
 Nakai K., Yada T., Nakamura Y., Ohara O., Isozaki T., Sugano S.,
 "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
 Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Bhat N.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Datchenko L., Maruska K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abtaman R.D., Mullaly S.J.,
 Bosak S., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahy J., Helton E., Ketterman M., Madan A.C., Rodriguez S., Sanchez A.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalski U., Smalios D.E., Scherch A., Schein J.E.,
 Jones S.J., Mair M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Straussberg R.,

Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 CC -1 Similarity: Belongs to the type-B carboxylesterase/11pase family.
 DR EMBL; AK056109; BAB71094.1; -
 DR EMBL; BC069548; AA069548.1; -
 DR HSSP; P12337; 1K4Y.
 DR GO; GO:0016787; F-hydrolase activity; IEA.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000379; Ser_esterase.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KM Hydrolase; Hypothetical protein.
 SQ SEQUENCE 525 AA; 58200 MW; 7724878B8A22F215 CRC64;

Query Match 68.8%; Score 400; DB 2; Length 525;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 GPSAGPQNRNRLGWIQGVTVVGSFVNVVFLGVPAAPPLGSLPFTNPQASPMDNT 90
 Db 25 GPSAGPQNRNRLGWIQGVTVVGSFVNVVFLGVPAAPPLGSLPFTNPQASPMDNT 84
 OY 91 REATSYPNLCIONSEMLLDQMLKVPKFGVSEDCYLYNTPAHADGSKLPVTVWF 150
 Db 85 REATSYPNLCIONSEMLLDQMLKVPKFGVSEDCYLYNTPAHADGSKLPVTVWF 144
 OY 151 PGAKRTSSAIFPGSALAAEDVLYVVOYRLGIFGFTTMDQAHAGNNAFKDOVAALS 210
 Db 145 PGAKRTSSAIFPGSALAAEDVLYVVOYRLGIFGFTTMDQAHAGNNAFKDOVAALS 204
 OY 211 WVKNIIEFFGDPSSVITFGESAGAISSVSLISPMKGLFHRNIMSSGVAIIPYLEAND 270
 Db 205 WVKNIIEFFGDPSSVITFGESAGAISSVSLISPMKGLFHRNIMSSGVAIIPYLEAND 264
 OY 271 YEKEDDQVNAHFGGNASDSEALRLCTRTPSKELLTTSOKTKSFTRVVDGAFPNNEPL 330
 Db 265 YEKEDDQVNAHFGGNASDSEALRLCTRTPSKELLTTSOKTKSFTRVVDGAFPNNEPL 324
 OY 331 DLSQKAFKAIPISTIGVNHCEGFLPMKEAPFISGSKSLALHLIQNIHLIPPOYLHL 390
 Db 325 DLSQKAFKAIPISTIGVNHCEGFLPMKEAPFISGSKSLALHLIQNIHLIPPOYLHL 384
 OY 391 VANEYFHDKSLTEIRDSLLDLGDVFFVVPALITARYR 430
 Db 385 VANEYFHDKSLTEIRDSLLDLGDVFFVVPALITARYR 424

RESULT 3

08NBC8 PRELIMINARY; PRT; 469 AA.
 AC 08NBC8; ID 08NBC8; DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ33678.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsura N., Sato K., Tanikawa M., Yamazaki M.,
 RA Nimomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kinata M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Houta T., Kubano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Tsujiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuki H., Oshima A., Sasaki N., Aotake S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Komiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Higashigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kusagaki A., Itakura S., Fukuzawa T.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujitara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki S., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Miushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RA "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs." ;
 RL Nat. Genet. 36:40-45(2004).
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL; AK090997; BAC03565.1; -.
 DR HSSP; P12337; 1K4Y.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR InterPro; IPR002018; Carbesterease.
 DR InterPro; IPR000379; Ser_esterase.
 DR Pfam; PF00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 DR KJ Hydrolyase.
 KW SEQUENCE 469 AA; 52312 MW; 7A18F68C10A9080 CRC64;

Query Match 56.6%; Score 329; DB 2; Length 469;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 429; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 1 MLKHYHPEKGVSEBDLYNITAPAPADTGSKLPVLWMPGGAFTGASIFDGSAALAYE 60

QY 173 DVLVVVVQYRIGIFGFTTMDQHPAGNMAFKDQVAAALSMVQNTIEFFGSDSSVTTFGES 232
 DB 61 DVLVVVVQYRIGIFGFTTMDQHPAGNMAFKDQVAAALSMVQNTIEFFGSDSSVTTFGES 120

QY 233 AGAIVSSSLIISPMAGKLFHKAINEGVAIIPYLEADHYEKSEDLQVVAHFCGNNAQSE 292
 DB 121 AGAIVSSSLIISPMAGKLFHKAINEGVAIIPYLEADHYEKSEDLQVVAHFCGNNAQSE 180

QY 293 ALLACLRKPKSEKLLTTSQKTSKFRVVDGAFPPPEPDLISQKAFKAPISLIGNNHNEC 352
 DB 181 ALLACLRKPKSEKLLTTSQKTSKFRVVDGAFPPPEPDLISQKAFKAPISLIGNNHNEC 240

QY 353 GFLPMKEAPEILSGSNKSLALHLQNLHLPQYLHLVANEYFPHDKSLTEIRDSLIDL 412
 DB 241 GFLPMKEAPEILSGSNKSLALHLQNLHLPQYLHLVANEYFPHDKSLTEIRDSLIDL 300

QY 413 LGDVFVVPALITARYHDAQAPVYFYEFRRPQCFFEDTKAFVKAHDADEVRFVGGAF 472
 DB 301 LGDVFVVPALITARYHDAQAPVYFYEFRRPQCFFEDTKAFVKAHDADEVRFVGGAF 360

QY 473 LKGDIVMEGATEBEKLSRKMMKWAFARTGNNGNDLSMPVYNLTBOYLQDLNMS 532
 DB 361 LKGDIVMEGATEBEKLSRKMMKWAFARTGNNGNDLSMPVYNLTBOYLQDLNMS 420

QY 533 LGORLKEPRV 542

DB 421 LGORLKEPRV 430

RESULT 4
 ID 095KH3 PRELIMINARY; PRT; 361 AA.
 AC 095KH3;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Macaca.
 NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Temporal lobe right;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Ieki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RL Submitted (ABR-2001) to the EMBL/GenBank/DDBJ databases.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL; AB060873; BAB6884.1; -.
 DR HSSP; P12337; 1K4Y.
 DR InterPro; IPR002018; Carbesterease.
 DR Pfam; PF00135; Coesterase; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 361 AA; 41032 MW; AC62AB6E78CF1A1 CRC64;

Query Match 17.4%; Score 101; DB 2; Length 361;
 Best Local Similarity 100.0%; Pred. No. 1; 5e-93;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 409 LLDLGDVFFVVPALITARYHDAQAPVYFYEFRRPQCFFEDTKAFVKAHDADEVRFV 468
 DB 183 LLDLGDVFFVVPALITARYHDAQAPVYFYEFRRPQCFFEDTKAFVKAHDADEVRFV 242

QY 469 GGAFLKGDIVMEGATEBEKLSRKMMKWAFARTGNPNP 509
 DB 243 GGAFLKGDIVMEGATEBEKLSRKMMKWAFARTGNPNP 283

RESULT 5
 ID 081034 PRELIMINARY; PRT; 545 AA.
 AC 081034;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Carboxylesterase-like urinary excreted protein.
 GN Name=Cauxin;
 OS Felis silvestris catus (Cat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA MEDLINE=22458314; PubMed=12401131; DOI=10.1042/BJ20021446;
 RA Miyazaki M., Kamie K., Soeta S., Taira H., Yamashita T.;
 RT "Molecular cloning and characterization of a novel carboxylesterase-
 RT like protein that is physiologically present at high concentrations in
 RT the urine of domestic cats (Felis catus).";
 RL Biochem. J. 370:101-110(2003).
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL; AB045377; BAC22577.1; -.
 DR HSSP; P12337; 1K4Y.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR InterPro; IPR002018; Carbesterease.
 DR InterPro; IPR000379; Ser_esterase.
 DR Pfam; PF00135; Coesterase; 1.

DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 545 AA; 60505 MW; 9F73FA693D271FA9 CRC64;

Query Match 5.3%; Score 31; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 4.4e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 459 RFVFGAFLKGDIVMFEGATEEEKLSRKM 489

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Job time : 181 secs

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OM protein - protein search, using BW model

Run on: June 16, 2005, 20:55:54 ; Search time 43 Seconds
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Title: US-10-674-636-2

Perfect score: 581
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size: 30

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	581	100.0	581	4	US-10-023-515-2 Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-10-023-515-2
; Sequence 2, Application US/10023515
; Patent No. 6664091
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYL ESTERASE
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 581
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-023-515-2

Query Match 100.0%; Score 581; DB 4; Length 581;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MPQGLTSSASQWCFLLIQPLIGHROWGKTGPSAEGQORNTLGMIGQKQVTVLGSPPV 60
Qy	61	NVFLGVPPAPPLGSLRFTNPQASPWDNIREATSYNNLCIONSEMLLDQMLKATPK 120
Db	61	NVFLGVPPAPPLGSLRFTNPQASPWDNIREATSYNNLCIONSEMLLDQMLKATPK 120
Qy	121	FGVSEDCLYNIVAPAHADGSKLPVLPVPPGAFKTSASIFDGSALAAVEDLVVVVQ 180
Db	121	FGVSEDCLYNIVAPAHADGSKLPVLPVPPGAFKTSASIFDGSALAAVEDLVVVVQ 180
Qy	181	YRLGIFGFPTTWDQAHGNNAFKQVVAALSVQKNIFFGSDPSSVTIFGSSAGASVSS 240
Db	181	YRLGIFGFPTTWDQAHGNNAFKQVVAALSVQKNIFFGSDPSSVTIFGSSAGASVSS 240
Qy	241	LIISPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAHFCGNNASDSEALLRCIRT 300
Db	241	LIISPMAKGLFHKAIMESGVAIIPYLEADHYEKSEDLQVVAHFCGNNASDSEALLRCIRT 300
Qy	301	KPSKELLTTSOKTSTFRVVDGAFEPNEPLDLSOKAFKAIPIIIGVNNHCGFLLPWKE 360
Db	301	KPSKELLTTSOKTSTFRVVDGAFEPNEPLDLSOKAFKAIPIIIGVNNHCGFLLPWKE 360
Qy	361	APETLSSGNSKSLAHLIQLNIHIPPQYLHLVANEYFHDKISLTERISLIDLGDVFEVV 420
Db	361	APETLSSGNSKSLAHLIQLNIHIPPQYLHLVANEYFHDKISLTERISLIDLGDVFEVV 420
Qy	421	PALITARYHRDAGAPVYFYEFRRHPQCFEDTKPAFVADHAEVRFVFGAFLKGDIVMF 480
Db	421	PALITARYHRDAGAPVYFYEFRRHPQCFEDTKPAFVADHAEVRFVFGAFLKGDIVMF 480
Qy	481	EGATEEEKLSRKKMKYATFARTGNPNDLSIWPAYNLTEQYLQDLNWSLQRLKEP 540
Db	481	EGATEEEKLSRKKMKYATFARTGNPNDLSIWPAYNLTEQYLQDLNWSLQRLKEP 540
Qy	541	RVDFTSTIPLILASDMLHSPSLTFLSLQPFPPFCAP 581
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Job time : 43 secs

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OM protein - protein search, using sw model

Run on: June 16, 2005, 21:02:21 ; Search time 159 Seconds
(without alignments)
1403.095 Million cell updates/sec

Title: US-10-674-636-2

Perfect score: 581

Sequence: 1 MPOGUTSSASQWCFEFLIOP.....PLSLTFLSLLOPPFFFCAP 581

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1714042 seqs, 383979560 residues

Word size : 30

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Published Applications_AA:*

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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10G_PUBCOMB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US10H_PUBCOMB.pep:*

21: /cgn2_6/ptodata/2/pubpaa/US10I_PUBCOMB.pep:*

22: /cgn2_6/ptodata/2/pubpaa/US10J_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	581	100.0	581	US-10-023-515-2	Sequence 2, Appl1
2	581	100.0	581	US-10-674-636-2	Sequence 2, Appl1
3	581	100.0	581	US-10-757-262-46	Sequence 46, Appl1
4	551	99.8	575	US-10-451-168-91	Sequence 91, Appl1
5	400	66.8	525	US-10-094-749-2375	Sequence 2375, Appl1
6	381	65.6	442	US-10-433-256-10	Sequence 10, Appl1
7	340	58.5	356	US-10-451-168-93	Sequence 93, Appl1
8	329	56.6	469	US-10-104-047-2219	Sequence 2219, Appl1
9	328	56.5	481	US-10-114-270-196	Sequence 196, Appl1
10	328	56.5	581	US-10-451-168-92	Sequence 92, Appl1
11	328	56.5	618	US-10-381-898-2	Sequence 2, Appl1

12	49	8.4	49	9	US-09-864-761-36376	Sequence 36376, A
13	31	5.3	542	16	US-10-233-933A-2	Sequence 2, Appl1
14	31	5.3	542	16	US-10-233-933A-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-10-023-515-2
Sequence 2, Application US/10023515
Publication No. US20020182636A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
TITLE OF INVENTION: Silos-Santiago, Immaculada
TITLE OF INVENTION: FAMILY MEMBER AND USRS THEROF
FILE REFERENCE: 10448-122001
CURRENT FILING DATE: US/10/023, 515
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq, for Windows Version 4.0
SEQ ID NO 2
LENGTH: 581
TYPE: PRT
ORGANISM: Homo sapiens
US-10-023-515-2

Query Match	100.0%	Score 581	DB 13	Length 581
Best Local Similarity	100.0%	Pred. No. 0		
Matches 581	Conservative 0	Mismatches 0	Indels 0	Gaps 0
1	MPOGUTSSASQWCFEFLIOPLLGHRQWKTGPSAEGPQRNRLGWIQKQVTVLGSPPV	60		
1	MPOGUTSSASQWCFEFLIOPLLGHRQWKTGPSAEGPQRNRLGWIQKQVTVLGSPPV	60		
61	NVFLGVPAAAPPLGSLRTNPQASPMONLEAATSYPLCQNSWMLLDHMLKVHPK	120		
61	NVFLGVPAAAPPLGSLRTNPQASPMONLEAATSYPLCQNSWMLLDHMLKVHPK	120		
121	FGVSEDCLYLNTIYAPAHADTSGKLPVLVWPFPGAFKTSASIFDGSALAAVEDVLVVVQ	180		
121	FGVSEDCLYLNTIYAPAHADTSGKLPVLVWPFPGAFKTSASIFDGSALAAVEDVLVVVQ	180		
181	YRLGIFGFTTMDQAPGNMAFKQVVALSWQKNIIEFGDPSSTVTFGSAGASIVSS	240		
181	YRLGIFGFTTMDQAPGNMAFKQVVALSWQKNIIEFGDPSSTVTFGSAGASIVSS	240		
241	LILSPMAKGLFHAKIMESGVAIIPYLEADYEKSEDLQVVAHFCGNNASDSBALRCIRT	300		
241	LILSPMAKGLFHAKIMESGVAIIPYLEADYEKSEDLQVVAHFCGNNASDSBALRCIRT	300		
301	KPSKELLTSLQKTSFTRVVDGAFEPNRLDLSOKAKAIPSTIGVNNHCEGFLPKME	360		
301	KPSKELLTSLQKTSFTRVVDGAFEPNRLDLSOKAKAIPSTIGVNNHCEGFLPKME	360		
361	APELLGSNKSALALHILIONIIHIPQYLAHVAEYFHDKSLTEIRDSILDLGDPFVV	420		
361	APELLGSNKSALALHILIONIIHIPQYLAHVAEYFHDKSLTEIRDSILDLGDPFVV	420		
421	PALITARYHRDAGAPVYFEFRHRPQCEDTKPAFKADHAEVRFVFGAFLKDIYWF	480		
421	PALITARYHRDAGAPVYFEFRHRPQCEDTKPAFKADHAEVRFVFGAFLKDIYWF	480		
481	EGATEEELSLSRKMKWATFARTGNPNGNDLSMPAYNLTEOYLQDLNMSIGORLKEP	540		
481	EGATEEELSLSRKMKWATFARTGNPNGNDLSMPAYNLTEOYLQDLNMSIGORLKEP	540		
541	RVDFWTSTIPLILSASDMILHSPLSLTFELSLLOPPFFFCAP 581			

Db 541 RVDFTSTTLPILISADMLHSPUSLTLFLSLQPFPPFCAP 581

```
RESULT 2
US-10-674-636-2
; Sequence 2: Application US/10674636
; Publication No. US20040086922A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/674,636
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/10/023,515
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-674-636-2
```

```
Query Match 100.0%; Score 581; DB 15; Length 581;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPOGLTSSASQWCFLLIQLPILGHRQWKGTPSAEGFORNTRLGWIQKQVTVLGSBPVPV 60
Db 1 MPOGLTSSASQWCFLLIQLPILGHRQWKGTPSAEGFORNTRLGWIQKQVTVLGSBPVPV 60
QY 61 NVFLGVFPFAAPPLGSLRFTNPQASPMNDNREATSVNCLQNSEWMLLDQHMLKTHYRK 120
Db 61 NVFLGVFPFAAPPLGSLRFTNPQASPMNDNREATSVNCLQNSEWMLLDQHMLKTHYRK 120
QY 121 FGVSIEDCLYNTIYAPAHADTGSKLPLVWMPGGAFTGSAIFDGSALAAVEDVLVVVQ 180
Db 121 FGVSIEDCLYNTIYAPAHADTGSKLPLVWMPGGAFTGSAIFDGSALAAVEDVLVVVQ 180
QY 121 YRLGIRFETFTTQOHAAGNMAFKDOVAALSWQKNIIEFGGDPSSVTIIGESAGAISVS 240
Db 121 YRLGIRFETFTTQOHAAGNMAFKDOVAALSWQKNIIEFGGDPSSVTIIGESAGAISVS 240
QY 181 YRLGIRFETFTTQOHAAGNMAFKDOVAALSWQKNIIEFGGDPSSVTIIGESAGAISVS 240
Db 181 YRLGIRFETFTTQOHAAGNMAFKDOVAALSWQKNIIEFGGDPSSVTIIGESAGAISVS 240
QY 241 LILSPMAKGLFHAKIMESGVAIIPYLEAHDYKSEDLQVVAHFCCGNAASDSEALLRCLRT 300
Db 241 LILSPMAKGLFHAKIMESGVAIIPYLEAHDYKSEDLQVVAHFCCGNAASDSEALLRCLRT 300
QY 301 KPSKELLITLSQKTKSFTRVVDGAFPNNEPLDLLSOKAFKAIPSIIGVNNHECGFLLPMKE 360
Db 301 KPSKELLITLSQKTKSFTRVVDGAFPNNEPLDLLSOKAFKAIPSIIGVNNHECGFLLPMKE 360
QY 361 APPIILSGNSKSLALHILIONILHITPQYLIHVANEYHHDGSLTETIDSLDLGLGVFFV 420
Db 361 APPIILSGNSKSLALHILIONILHITPQYLIHVANEYHHDGSLTETIDSLDLGLGVFFV 420
QY 421 PALITARYHRDAGAPYFYEFRHRPQCFEDTKPAFAKADHADEVRFVFGAFLKGDYWF 480
Db 421 PALITARYHRDAGAPYFYEFRHRPQCFEDTKPAFAKADHADEVRFVFGAFLKGDYWF 480
QY 481 EGATEBEKLSRKMMKYATFARTGNPNDLSLWPAYNLTEQYQLDLNMSLGRLEK 540
Db 481 EGATEBEKLSRKMMKYATFARTGNPNDLSLWPAYNLTEQYQLDLNMSLGRLEK 540
QY 541 RVDFTSTTLPILISADMLHSPUSLTLFLSLQPFPPFCAP 581
Db 541 RVDFTSTTLPILISADMLHSPUSLTLFLSLQPFPPFCAP 581
```

```
RESULT 3
US-10-757-262-46
; Sequence 46: Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheh, Venkateswarlu
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Eliaouf, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 16560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 22077, 22245, 2387, 52308, 69112, 14990,
; TITLE OF INVENTION: 16547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; FILE REFERENCE: MP103-007P1RNMNM
; CURRENT APPLICATION NUMBER: US/10/757,262
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-46

Query Match 100.0%; Score 581; DB 16; Length 581;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPOGLTSSASQWCFLLIQLPILGHRQWKGTPSAEGFORNTRLGWIQKQVTVLGSBPVPV 60
Db 1 MPOGLTSSASQWCFLLIQLPILGHRQWKGTPSAEGFORNTRLGWIQKQVTVLGSBPVPV 60
QY 61 NVFLGVFPFAAPPLGSLRFTNPQASPMNDNREATSVNCLQNSEWMLLDQHMLKTHYRK 120
Db 61 NVFLGVFPFAAPPLGSLRFTNPQASPMNDNREATSVNCLQNSEWMLLDQHMLKTHYRK 120
QY 121 FGVSIEDCLYNTIYAPAHADTGSKLPLVWMPGGAFTGSAIFDGSALAAVEDVLVVVQ 180
Db 121 FGVSIEDCLYNTIYAPAHADTGSKLPLVWMPGGAFTGSAIFDGSALAAVEDVLVVVQ 180
QY 181 YRLGIRFETFTTQOHAAGNMAFKDOVAALSWQKNIIEFGGDPSSVTIIGESAGAISVS 240
Db 181 YRLGIRFETFTTQOHAAGNMAFKDOVAALSWQKNIIEFGGDPSSVTIIGESAGAISVS 240
QY 241 LILSPMAKGLFHAKIMESGVAIIPYLEAHDYKSEDLQVVAHFCCGNAASDSEALLRCLRT 300
Db 241 LILSPMAKGLFHAKIMESGVAIIPYLEAHDYKSEDLQVVAHFCCGNAASDSEALLRCLRT 300
```


Db 241 LILSPMAKGLFHKAIMESGVAIIIPYLEAHDIYEKSEDLQVVAHFCGNNADEBALRCLRT 300
Qy 301 KPSKELLTISQKTSFTRVVDGAFEPNEPLDLSQAKFAIPSIIGVNNHCGFLLPKME 360
Db 301 KPSKELLTISQKTSFTRVVDGAFEPNEPLDLSQAKFAIPSIIGVNNHCGFLLPKME 360
Qy 361 APEILSGSNKSLAHLIIONIIHIPQYHLVANEXFHDKSLTEIRDSLLDLGDFVIV 420
Db 361 APEILSGSNKSLAHLIIONIIHIPQYHLVANEXFHDKSLTEIRDSLLDLGDFVIV 420
Qy 421 PALTARHRAAGAPVYFEFRHRPQCEBDTKPAVKADHDEVRFVGCAPFLKGDIMF 480
Db 421 PALTARHRAAGAPVYFEFRHRPQCEBDTKPAVKADHDEVRFVGCAPFLKGDIMF 480
Qy 481 EGATEEBEKLRSKMKMYATFARTGNPNDLSLMPAYNLTEOYLQDLNMSLQRLKEP 540
Db 481 EGATEEBEKLRSKMKMYATFARTGNPNDLSLMPAYNLTEOYLQDLNMSLQRLKEP 540
Qy 541 RVDFWTSTIPIILSASDMLHSPLSLFTLSLQPPFFCAP 581
Db 541 RVDFWTSTIPIILSASDMLHSPLSLFTLSLQPPFFCAP 581

RESULT 4

US-10-451-168-91
Sequence 91, Application US/10451168
Publication No. US20040091969A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 91
LENGTH: 575
TYPE: PRT
ORGANISM: Homo sapiens
US-10-451-168-91

Query Match 94.8%; Score 551; DB 15; Length 575;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 GPSAGPQNRTRLGWIQGVQVTVLGSVPVNVFLGVPAAPLGSRLFTNPQASPMDNL 90
Db 25 GPSAGPQNRTRLGWIQGVQVTVLGSVPVNVFLGVPAAPLGSRLFTNPQASPMDNL 84
Qy 91 REATSYVULCLONSWLLLDQMLKVHYPKRGVSEDCLYNIYAAHADTGSKLPLYLWF 150
Db 85 REATSYVULCLONSWLLLDQMLKVHYPKRGVSEDCLYNIYAAHADTGSKLPLYLWF 144

Qy 151 PGCAFXTGSASIFRGSALAAVEDLVVVVVOYRLGI FGPFRTWDDHAPGNMAFKQVVALS 210
Db 145 PGCAFXTGSASIFRGSALAAVEDLVVVVVOYRLGI FGPFRTWDDHAPGNMAFKQVVALS 204
Qy 211 MVQNIIEFGDPSPVITFGESAGAISSVSLISPMKGLFHKAIMESGVAIIIPYLEAND 270
Db 205 MVQNIIEFGDPSPVITFGESAGAISSVSLISPMKGLFHKAIMESGVAIIIPYLEAND 264
Qy 271 YEKSEDLQVVAHFCGNNADEBALRCLRTKPSKELLTISQKTSFTRVVDGAFEPNEPL 330
Db 265 YEKSEDLQVVAHFCGNNADEBALRCLRTKPSKELLTISQKTSFTRVVDGAFEPNEPL 324
Qy 331 DLSQAKFAIPSIIGVNNHCGFLLPKMEPEILSGSNKSLAHLIIONIIHIPQYHL 390
Db 325 DLSQAKFAIPSIIGVNNHCGFLLPKMEPEILSGSNKSLAHLIIONIIHIPQYHL 384
Qy 391 VANEPFHDKSLTEIRDSLLDLGDFVIVPALTARHRAAGAPVYFEFRHRPQCEBD 450
Db 385 VANEPFHDKSLTEIRDSLLDLGDFVIVPALTARHRAAGAPVYFEFRHRPQCEBD 444
Qy 451 TKPAFVADHDEVRFVGCAPFLKGDIMFEGATEEBEKLRSKMKMYATFARTGNPND 510
Db 445 TKPAFVADHDEVRFVGCAPFLKGDIMFEGATEEBEKLRSKMKMYATFARTGNPND 504
Qy 511 DLSMPAYNLTEOYLQDLNMSLQRLKEPVDFTWTSTIPIILSASDMLHSPLSLFTLS 570
Db 505 DLSMPAYNLTEOYLQDLNMSLQRLKEPVDFTWTSTIPIILSASDMLHSPLSLFTLS 564
Qy 571 LLOPPFFCAP 581
Db 565 LLOPPFFCAP 575

RESULT 5

US-10-094-749-2375
Sequence 2375, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKU
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2375
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2375

Query Match 68.8%; Score 400; DB 15; Length 525;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GSAAGPQNRTRLGMIOGKQVTVLGSFVFNFLGVFAAPPLGSLRFTNPPASPMNDL 90
DB 25 GSAAGPQNRTRLGMIOGKQVTVLGSFVFNFLGVFAAPPLGSLRFTNPPASPMNDL 84
QY 91 REATSYPNICLQNSEWMLLDQHLKVHYPKFVSEDCLYLNIYAPAHADTGSKLPLYWVF 150
DB 85 REATSYPNICLQNSEWMLLDQHLKVHYPKFVSEDCLYLNIYAPAHADTGSKLPLYWVF 144
QY 151 PGAFKTSASIFDGSALAAVEDLVVVOYRLGIFGFPTTWDQAPGNMAFKDOVALS 210
DB 145 PGAFKTSASIFDGSALAAVEDLVVVOYRLGIFGFPTTWDQAPGNMAFKDOVALS 204
QY 211 WQKNIIEFGDPSSVTIFGESAGAISSVSLISPMAGLPHKAIMESGVAIIPYLEAHD 270
DB 205 WQKNIIEFGDPSSVTIFGESAGAISSVSLISPMAGLPHKAIMESGVAIIPYLEAHD 264
QY 271 YEKSEDLQVVAHFCGNMNSDEBALRLCRLTPKSKELLTISOXTKSFTRVVDGAFPPNEPL 330
DB 265 YEKSEDLQVVAHFCGNMNSDEBALRLCRLTPKSKELLTISOXTKSFTRVVDGAFPPNEPL 324
QY 331 DLSQKAFKAIPIIIGVNNHECGFLLPMKEAPEILSGNSKSLAHLQNIILHIIPQYVHL 390
DB 325 DLSQKAFKAIPIIIGVNNHECGFLLPMKEAPEILSGNSKSLAHLQNIILHIIPQYVHL 384
QY 391 VANEFYHDKSLTEIRDSLLDLGDFVFPVPAITARYHR 430
DB 385 VANEFYHDKSLTEIRDSLLDLGDFVFPVPAITARYHR 424

RESULT 6

US-10-433-256-10
Sequence 10, Application US/10433256
Publication No. US20040081980A1
GENERAL INFORMATION:
APPLICANT: SANJANMALA, Madhusudan M.; YAO, Monique G.
APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R.
APPLICANT: ARVIZU, Chandra S.; KING, Huijun Z.
APPLICANT: LEE, Ernestine A.; DING, Li
APPLICANT: HAPALIA, April J.A.; TANG, Y. Tom
APPLICANT: YUE, Henry; TRIBOULEY, Catherine M.
APPLICANT: LU, Dying; ALINA M.; LAL, Preci G.
APPLICANT: WARREN, Bridget A.; YANG, Junming
APPLICANT: CHAWLA, Narinder K.; NGUYEN, Daniel B.
APPLICANT: GANDHI, Ameena R.; LU, Yan
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0313 USN
CURRENT APPLICATION NUMBER: US/10/433,256
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: PCT/US01/47429
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/256,189
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 642
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 6538080CD1

US-10-433-256-10

Query Match 65.6%; Score 381; DB 15; Length 642;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 481; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 31 GSAAGPQNRTRLGMIOGKQVTVLGSFVFNFLGVFAAPPLGSLRFTNPPASPMNDL 90
DB 92 GSAAGPQNRTRLGMIOGKQVTVLGSFVFNFLGVFAAPPLGSLRFTNPPASPMNDL 151
QY 91 REATSYPNICLQNSEWMLLDQHLKVHYPKFVSEDCLYLNIYAPAHADTGSKLPLYWVF 150
DB 152 REATSYPNICLQNSEWMLLDQHLKVHYPKFVSEDCLYLNIYAPAHADTGSKLPLYWVF 211
QY 151 PGAFKTSASIFDGSALAAVEDLVVVOYRLGIFGFPTTWDQAPGNMAFKDOVALS 271
DB 212 PGAFKTSASIFDGSALAAVEDLVVVOYRLGIFGFPTTWDQAPGNMAFKDOVALS 271
QY 211 WQKNIIEFGDPSSVTIFGESAGAISSVSLISPMAGLPHKAIMESGVAIIPYLEAHD 270
DB 272 WQKNIIEFGDPSSVTIFGESAGAISSVSLISPMAGLPHKAIMESGVAIIPYLEAHD 331
QY 271 YEKSEDLQVVAHFCGNMNSDEBALRLCRLTPKSKELLTISOXTKSFTRVVDGAFPPNEPL 330
DB 332 YEKSEDLQVVAHFCGNMNSDEBALRLCRLTPKSKELLTISOXTKSFTRVVDGAFPPNEPL 391
QY 331 DLSQKAFKAIPIIIGVNNHECGFLLPMKEAPEILSGNSKSLAHLQNIILHIIPQYVHL 390
DB 392 DLSQKAFKAIPIIIGVNNHECGFLLPMKEAPEILSGNSKSLAHLQNIILHIIPQYVHL 451
QY 391 VANEFYHDKSLTEIRDSLLDLGDFVFPVPAITARYHRDAGAPVYFEFRHRPOCED 450
DB 452 VANEFYHDKSLTEIRDSLLDLGDFVFPVPAITARYHRDAGAPVYFEFRHRPOCED 511
QY 451 TKPAFVKADHDEVFVFGAFGLKGDITMEGATBEELSRKMKWATFARTGNNGN 510
DB 512 TKPAFVKADHDEVFVFGAFGLKGDITMEGATBEELSRKMKWATFARTGNNGN 571
QY 511 DL 512
DB 572 DL 573

RESULT 7

US-10-451-168-93
Sequence 93, Application US/10451168
Publication No. US20040091969A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.L.C.
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 93
LENGTH: 356
TYPE: PRT
ORGANISM: Homo sapiens
US-10-451-168-93

Query Match 58.5%; Score 340; DB 15; Length 356;
Best Local Similarity 100.0%; Pred. No. 3,4e-313;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 ILSPMAKGLFHKAIMESGVAIIPLYLAHDYKESDLOVVAHFCGNNASDSEALRLCLRTK 301
DB 17 ILSPMAKGLFHKAIMESGVAIIPLYLAHDYKESDLOVVAHFCGNNASDSEALRLCLRTK 76
QY 302 PSKELLTTSQRTKSTRVVDGAFPPNEPLDLSQKAFKAIPIIIGVNHCEGFLPMKEA 361
DB 77 PSKELLTTSQRTKSTRVVDGAFPPNEPLDLSQKAFKAIPIIIGVNHCEGFLPMKEA 136
QY 362 PEILSGNKSIALHLIQLNIHLIPQYLHLVANEYFHDKSLTEIRDSLLDLGDFVFPVP 421
DB 137 PEILSGNKSIALHLIQLNIHLIPQYLHLVANEYFHDKSLTEIRDSLLDLGDFVFPVP 196
QY 422 ALITARYHDAGAPVYFYEFRHRPOCFEDTKPAFYKADHAEVRFVFGAFLKGDIVME 481
DB 197 ALITARYHDAGAPVYFYEFRHRPOCFEDTKPAFYKADHAEVRFVFGAFLKGDIVME 256
QY 482 GATEBEKLSRKMKYATFARTGNPNNDLSLMPAYNLTEQYLOLDLMSIGORLKEPR 541
DB 257 GATEBEKLSRKMKYATFARTGNPNNDLSLMPAYNLTEQYLOLDLMSIGORLKEPR 316
QY 542 VDFMTSTPLILSASDMHSPSLTFLSLLOPFFFCAP 581
DB 317 VDFMTSTPLILSASDMHSPSLTFLSLLOPFFFCAP 356

RESULT 8
US-10-104-047-2219
Sequence 2219, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1 full length cDNA
FILE REFERENCE: HI-A0105
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: US/10/104,047
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2219
LENGTH: 469
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-2219

Query Match 56.6%; Score 329; DB 15; Length 469;
Best Local Similarity 99.8%; Pred. No. 1.1e-302;
Matches 429; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 113 MLKHYPRFGVSEDCLYNITYAPADTGSKLPVLVWFGGAFKTSASIFDGSALAYE 172
DB 1 MLKHYPRFGVSEDCLYNITYAPADTGSKLPVLVWFGGAFKTSASIFDGSALAYE 60
QY 173 DVLVVVVYRLGIFGFTTWDQAHAGNNAFKDQVVALSWQKNIEFFGGDPSSVTIFGS 232
DB 61 DVLVVVVYRLGIFGFTTWDQAHAGNNAFKDQVVALSWQKNIEFFGGDPSSVTIFGS 120
QY 233 AGAIVSSILISPMKGLFHKAIMESGVAIIPLYLAHDYKESDLOVVAHFCGNNASDSE 292
DB 121 AGAIVSSILISPMKGLFHKAIMESGVAIIPLYLAHDYKESDLOVVAHFCGNNASDSE 180

QY 293 ALRLCLRTKPSKELLTTSQRTKSTRVVDGAFPPNEPLDLSQKAFKAIPIIIGVNHCE 352
DB 181 ALRLCLRTKPSKELLTTSQRTKSTRVVDGAFPPNEPLDLSQKAFKAIPIIIGVNHCE 240
QY 353 GFLPMKEAPRILSGNKSIALHLIQLNIHLIPQYLHLVANEYFHDKSLTEIRDSLLDL 412
DB 241 GFLPMKEAPRILSGNKSIALHLIQLNIHLIPQYLHLVANEYFHDKSLTEIRDSLLDL 300
QY 413 LGDFVFPVVALITARYHDAGAPVYFYEFRHRPOCFEDTKPAFYKADHAEVRFVFGAF 472
DB 301 LGDFVFPVVALITARYHDAGAPVYFYEFRHRPOCFEDTKPAFYKADHAEVRFVFGAF 360
QY 473 LKGDIVMEGATEBEKLSRKMKYATFARTGNPNNDLSLMPAYNLTEQYLOLDLMS 532
DB 361 LKGDIVMEGATEBEKLSRKMKYATFARTGNPNNDLSLMPAYNLTEQYLOLDLMS 420
QY 533 LGORLKEPRV 542
DB 421 LGORLKEPRV 430

RESULT 9
US-10-114-270-196
Sequence 196, Application US/10114270
Publication No. US20040030110A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Rameesh
APPLICANT: Miller, Charles E.
APPLICANT: Malysankar, Uriel M.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
APPLICANT: Liu, Zhaozhong
APPLICANT: Gusev, Vladimyr Y.
APPLICANT: Li, Li
APPLICANT: Verneet, Corrine
APPLICANT: Zethusen, Bryan D.
APPLICANT: Gorman, Linda
APPLICANT: Shenoy, Suresh G.
APPLICANT: Pena, Carol E.A.
APPLICANT: Smithson, Glenda
APPLICANT: Burgess, Catherine E.
APPLICANT: Gerlach, Valerie
APPLICANT: Padigaru, Muralidhara
APPLICANT: Shinkets, Richard A.
APPLICANT: Gangolli, Esba A.
APPLICANT: Taupier JF., Raymond J.
APPLICANT: Caeman, Stacie J.
APPLICANT: Ji, Weizhen
APPLICANT: Anderson, David W.
APPLICANT: Liete, Mario W.
APPLICANT: Raestelli, Luca
APPLICANT: Edinger, Shlomit R.
APPLICANT: Stone, David J.
APPLICANT: MacDougall, John R.
APPLICANT: Rothenberg, Mark E.
TITLE OF INVENTION: No. US20040030110A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-322C
CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,930
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/282,934

PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,512
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SEQ ID NO 196
LENGTH: 581
TYPE: PRT
ORGANISM: Homo sapiens
US-10-114-270-196

Query Match 56.5%; Score 328; DB 15; Length 581;
Best Local Similarity 100.0%; Pred. No. 1.2e-301;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GPSAEGQRTNTRIGWIGKQVTVLGSPPVNVFLGVPAPPLGSLRFTNPQPASPMNDL 90
DB 27 GPSAEGQRTNTRIGWIGKQVTVLGSPPVNVFLGVPAPPLGSLRFTNPQPASPMNDL 86
QY 91 REATSYPNCLQNSEWLLDDQHLKVHYPKFGVSEDCLYINITYAPAHADTGSKLPVLWF 150
DB 87 REATSYPNCLQNSEWLLDDQHLKVHYPKFGVSEDCLYINITYAPAHADTGSKLPVLWF 146
QY 151 PGGAFTGASIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQHPGNMAFKQVVALS 210
DB 147 PGGAFTGASIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQHPGNMAFKQVVALS 206
QY 211 WYQKNIFFGDPSSVTTFGESAGAISSVSLILSPMAKGLFHKAIMESGVAILPYLEBAHD 270
DB 207 WYQKNIFFGDPSSVTTFGESAGAISSVSLILSPMAKGLFHKAIMESGVAILPYLEBAHD 266
QY 271 YKSEDLQVVAHFCGNMNSDSEALLRCLRTKPSKELLTISOXTKSFTRVVDGAFFPNEPL 330
DB 267 YKSEDLQVVAHFCGNMNSDSEALLRCLRTKPSKELLTISOXTKSFTRVVDGAFFPNEPL 326
QY 331 DLSQAKFAKAIPIIIGVNNHCGFLPM 358
DB 327 DLSQAKFAKAIPIIIGVNNHCGFLPM 354

RESULT 10
US-10-451-168-92
Sequence 92, Application US/10451168
Publication No. US20040091969A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.L.C.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GPS0039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622

PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 92
LENGTH: 581
TYPE: PRT
ORGANISM: Homo sapiens
US-10-451-168-92

Query Match 56.5%; Score 328; DB 15; Length 581;
Best Local Similarity 100.0%; Pred. No. 1.2e-301;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GPSAEGQRTNTRIGWIGKQVTVLGSPPVNVFLGVPAPPLGSLRFTNPQPASPMNDL 90
DB 25 GPSAEGQRTNTRIGWIGKQVTVLGSPPVNVFLGVPAPPLGSLRFTNPQPASPMNDL 84
QY 91 REATSYPNCLQNSEWLLDDQHLKVHYPKFGVSEDCLYINITYAPAHADTGSKLPVLWF 150
DB 85 REATSYPNCLQNSEWLLDDQHLKVHYPKFGVSEDCLYINITYAPAHADTGSKLPVLWF 144
QY 151 PGGAFTGASIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQHPGNMAFKQVVALS 210
DB 145 PGGAFTGASIFDGSALAAVEDVLVVVQYRLGIFGFTTWDQHPGNMAFKQVVALS 204
QY 211 WYQKNIFFGDPSSVTTFGESAGAISSVSLILSPMAKGLFHKAIMESGVAILPYLEBAHD 270
DB 205 WYQKNIFFGDPSSVTTFGESAGAISSVSLILSPMAKGLFHKAIMESGVAILPYLEBAHD 264
QY 271 YKSEDLQVVAHFCGNMNSDSEALLRCLRTKPSKELLTISOXTKSFTRVVDGAFFPNEPL 330
DB 265 YKSEDLQVVAHFCGNMNSDSEALLRCLRTKPSKELLTISOXTKSFTRVVDGAFFPNEPL 324
QY 331 DLSQAKFAKAIPIIIGVNNHCGFLPM 358
DB 325 DLSQAKFAKAIPIIIGVNNHCGFLPM 352

RESULT 11
US-10-381-898-2
Sequence 2, Application US/10381898
Publication No. US2004008687A1
GENERAL INFORMATION:
APPLICANT: AZIMZAI, Yalda; BAUGHN, Mariah R.;
APPLICANT: BOROMSKY, Mark L.; DING, Li;
APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.;
APPLICANT: GANDHI, Ameena R.; GRIFFIN, Jennifer A.;
APPLICANT: HAPALIA, April J.A.; ISON, Craig H.;
APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;
APPLICANT: LEE, Ernestine A.; LU, Dyung Alina M.;
APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
APPLICANT: SANJANWALA, Madhusudan M.;
APPLICANT: TANG, Y. Tom; TRIBUNEY, Catherine M.;
APPLICANT: CHAWLA, Narinder K.; WALSH, Roderick T.;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: YANG, Junning; YAO, Monique; YUE, Henry
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0233 USN
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/US01/30662
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,947
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/238,864
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/242,323
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR FILING DATE: 2000-11-16

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;; PRIOR APPLICATION NUMBER: US 60/252,834
;; PRIOR FILING DATE: 2000-11-22
;; PRIOR APPLICATION NUMBER: US 60/250,567
;; PRIOR FILING DATE: 2000-11-30
;; NUMBER OF SEQ ID NOS: 36
;; SOFTWARE: PERL Program
;; SEQ ID NO 2
;; LENGTH: 618
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No: 7473645CD1
US-10-381-898-2

Query Match      56.5%; Score 328; DB 15; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.3e-301;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 GPSAEGPQNRTRLGMIOGKQVTVLGSPPVNVNVLGVPFAAPLGLSRTNPQASPMDNL 90
Db 92 GPSAAGPQNRTRLGMIOGKQVTVLGSPPVNVNVLGVPFAAPLGLSRTNPQASPMDNL 151
Qy 91 REATSYPMULCLQNSWMLLDQMLKVHYPKFGVSDCLYLNITYAPAHADTGSKLPLYWF 150
Db 152 REATSYPMULCLQNSWMLLDQMLKVHYPKFGVSDCLYLNITYAPAHADTGSKLPLYWF 211
Qy 151 PGGAFTKSASTFDGSAALAAVEDVAVVVQVRLGIFGFFTTMDQHPGNNMAFKDQVAALS 210
Db 212 PGGAFTKSASTFDGSAALAAVEDVAVVVQVRLGIFGFFTTMDQHPGNNMAFKDQVAALS 271
Qy 211 WVKNIIEFFGDPSSVTIFGESAGATSVSSLLISPMAGLFFKAIMESGVALIPLYEAHD 270
Db 212 WVKNIIEFFGDPSSVTIFGESAGATSVSSLLISPMAGLFFKAIMESGVALIPLYEAHD 331
Qy 271 YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTISOXTKSFTRVVDGAFPPNEPL 330
Db 332 YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTISOXTKSFTRVVDGAFPPNEPL 391
Qy 331 DLLSOKAFKATPSITIGVNNHCEGFLPM 358
Db 392 DLLSOKAFKATPSITIGVNNHCEGFLPM 419

RESULT 12
US-09-864-761-36376
;; Sequence 36376, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wenheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aecmiga-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
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;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 36376
;; LENGTH: 49
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC007335.2
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.5
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.1
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.4
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
;; OTHER INFORMATION: EST HUMAN HIT: AV650422.1, EVALU8 2.00e-09
;; OTHER INFORMATION: SWISSPROT HIT: Q04791, EVALU8 2.00e-11
US-09-864-761-36376

Query Match      8.4%; Score 49; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 3.5e-38;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 432 AGAPYFYEFRRHPQCFEDTYPAPVKAHDADVRVFGGATLKGDVWF 480
Db 1 AGAPYFYEFRRHPQCFEDTYPAPVKAHDADVRVFGGATLKGDVWF 49

RESULT 13
US-10-233-933A-2
;; Sequence 2, Application US/10233933A
;; Publication No. US20040214171A1
;; GENERAL INFORMATION:
;; APPLICANT: Yamashita, Tecuero
;; APPLICANT: Miyazaki, Maeko
;; TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
;; FILE REFERENCE: SHIG FPO2US006
;; CURRENT APPLICATION NUMBER: US/10/233,933A
;; CURRENT FILING DATE: 2002-09-03
;; PRIOR APPLICATION NUMBER: JP2002-057908
;; PRIOR FILING DATE: 2002-04-03
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 542
;; TYPE: PRT
;; ORGANISM: Felis catus
US-10-233-933A-2
```

Query Match 5.3%; Score 31; DB 16; Length 542;
Best Local Similarity 100.0%; Pred. No. 3.4e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 465 RFVFGAFLKGDIVMEGATEEELLSRKM 495
DB 456 RFVFGAFLKGDIVMEGATEEELLSRKM 486

RESULT 14

US-10-233-933A-4
; Sequence 4, Application US/10233933A
; Publication No. US20040214171A1
; GENERAL INFORMATION:
; APPLICANT: Yamashita, Tetsuro
; APPLICANT: Miyazaki, Masao
; TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
; FILE REFERENCE: SHIG FP02US006
; CURRENT APPLICATION NUMBER: US/10/233,933A
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: JP2002-057908
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 542
; TYPE: PRF
; ORGANISM: Felis catus
US-10-233-933A-4

Query Match 5.3%; Score 31; DB 16; Length 542;
Best Local Similarity 100.0%; Pred. No. 3.4e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 465 RFVFGAFLKGDIVMEGATEEELLSRKM 495
DB 456 RFVFGAFLKGDIVMEGATEEELLSRKM 486

Search completed: June 16, 2005, 21:18:08
Job time : 160 secs